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(57) Abstract

By this invention, novel nucleic acid sequences encoding for acyltransferase related proteins are provided, wherein said acyltransferase–like protein is active in the transfer of a fatty acyl group from a fatty acyl donor to a fatty acyl acceptor. Also considered are amino acid and nucleic acid sequences obtainable from AT–like nucleic acid sequences and the use of such sequences to provide transgenic host cells capable of producing modified lipid content and composition.

NOVEL PLANT ACYLTRANSFERASES

INTRODUCTION

This application claims the benefit of U.S. Provisional Application Serial No. 60/101,939 filed September 25, 1998.

Technical Field

The present invention is directed to nucleic acid and amino acid sequences and constructs, and methods related thereto.

Background

Through the development of plant genetic engineering techniques, it is now possible to produce transgenic varieties of plant species to provide plants which have novel and desirable characteristics. For example, it is now possible to genetically engineer plants for tolerance to environmental stresses, such as resistance to pathogens and tolerance to herbicides and to improve the quality characteristics of the plant, for example improved fatty acid compositions. However, the number of useful nucleotide sequences for the engineering of such characteristics is thus far limited and the speed with which new useful nucleotide sequences for engineering new characteristics is slow.

The characterization of various acyltransferase proteins is useful for the further study of plant fatty acid synthesis systems and for the development of novel and/or alternative oils sources. Studies of plant mechanisms may provide means to further enhance, control, modify, or otherwise alter the total fatty acyl composition of triglycerides and oils. Furthermore, the elucidation of the factor(s) critical to the natural production of fatty acids in plants is desired, including the purification of such factors and the characterization of element(s) and/or cofactors which enhance the efficiency of the system. Of particular interest are the nucleic acid sequences of genes encoding proteins which may be useful for applications in genetic engineering.

SUMMARY OF THE INVENTION

5   The present invention provides nucleic acid encoding for amino acid sequences for a class of proteins which are related to acyltransferase proteins. Such proteins are referred to herein as acyltransferase related or acyltransferase like proteins.

By this invention, nucleic acid sequences encoding these acyltransferase related proteins may now be characterized with respect to enzyme activity. In particular,

10   identification and isolation of nucleic acid sequences encoding for acyltransferase related proteins from *Arabidopsis*, yeast, corn, and soybean are provided.

Thus, this invention encompasses acyltransferase related nucleic acid sequences and the corresponding amino acid sequences, and the use of these nucleic acid sequences in the preparation of oligonucleotides containing such acyltransferase related encoding sequences

15   for analysis and recovery of plant acyltransferase related gene sequences. The acyltransferase related encoding sequence may encode a complete or partial sequence depending upon the intended use. All or a portion of the genomic sequence, or cDNA sequence, is intended.

Of special interest are recombinant DNA constructs which provide for transcription or transcription and translation (expression) of the acyltransferase related sequences in host

20   cells. In particular, constructs which are capable of transcription or transcription and translation in plant host cells are preferred. For some applications a reduction in sequences encoding acyltransferase related sequences may be desired. Thus, recombinant constructs may be designed having the acyltransferase related sequences in a reverse orientation for expression of an anti-sense sequence or use of co-suppression, also known as "transwitch",

25   constructs may be useful. Such constructs may contain a variety of regulatory regions including transcriptional initiation regions obtained from genes preferentially expressed in plant seed tissue. For some uses, it may be desired to use the transcriptional and translational initiation regions of the acyltransferase related gene either with the acyltransferase related encoding sequence or to direct the transcription and translation of a heterologous sequence.

30   Also considered in this invention are the plants and seeds containing the constructs and polynucleotides of this invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides the 204 amino acid conserved sequence profile identified from comparisons of glycerol-3-phosphate acyltransferase and various lysophosphatidic acid acyltransferase using PSI-BLAST.

Figure 2 provides an amino acid sequence alignment for the acyltransferase sequences. The alignment shown is of the regions of the protein extending from about 30 amino acids prior to the conserved H in the conserved sequence HXXXXD to 100 amino acids after, or downstream, of the P in the conserved PEG sequence motif of the acyltransferase-like sequences.

Figure 3 provides schematics showing the relationship of the identified acyltransferases. The relationships described are derived from an alignment of the regions of the protein extending from about 30 amino acids prior to the conserved H in the conserved sequence HXXXXD to 100 amino acids after, or downstream, of the P in the conserved PEG sequence motif of the acyltransferase-like sequences. Figure 3A provide a phylogenetic tree showing the relationship of several acyltransferases. Figure 3B provides a table showing the percent similarities and percent divergence of the novel acyltransferases and known acyltransferases using the Clustal method with PAM250 residue weight table.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the subject invention, nucleotide sequences are provided which are capable of coding sequences of amino acids, such as, a protein, polypeptide or peptide, which are related to nucleic acid sequences encoding acyltransferase proteins, referred to herein as acyltransferase-like or acyltransferase related. The novel nucleic acid sequences find use in the preparation of constructs to direct their expression in a host cell. Furthermore, the novel nucleic acid sequences may find use in the preparation of plant expression constructs to modify the fatty acid composition of a plant cell.

In one embodiment of the present invention, nucleic acid sequences, also referred to herein as polynucleotides, are identified from databases which are related to acyltransferases.

Isolated proteins, Polypeptides and Polynucleotides

A first aspect of the present invention relates to isolated acyltransferase polynucleotides. The polynucleotide sequences of the present invention include isolated polynucleotides that encode the polypeptides of the invention having a deduced amino acid sequence selected from the group of sequences set forth in the Sequence Listing and to other polynucleotide sequences closely related to such sequences and variants thereof.

The invention provides a polynucleotide sequence identical over its entire length to each coding sequence as set forth in the Sequence Listing. The invention also provides the coding sequence for the mature polypeptide or a fragment thereof, as well as the coding sequence for the mature polypeptide or a fragment thereof in a reading frame with other coding sequences, such as those encoding a leader or secretory sequence, a pre-, pro-, or prepro- protein sequence. The polynucleotide can also include non-coding sequences, including for example, but not limited to, non-coding 5' and 3' sequences, such as the transcribed, untranslated sequences, termination signals, ribosome binding sites, sequences that stabilize mRNA, introns, polyadenylation signals, and additional coding sequence that encodes additional amino acids. For example, a marker sequence can be included to facilitate the purification of the fused polypeptide. Polynucleotides of the present invention also include polynucleotides comprising a structural gene and the naturally associated sequences that control gene expression.

The invention also includes polynucleotides of the formula:

$$X-(R_1)_n-(R_2)-(R_3)_n-Y$$
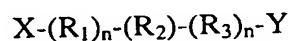
wherein, at the 5' end, X is hydrogen, and at the 3' end, Y is hydrogen or a metal, R_1 and R_3 are any nucleic acid residue, n is an integer between 1 and 3000, preferably between 1 and 1000 and R_2 is a nucleic acid sequence of the invention, particularly a nucleic acid sequence selected from the group set forth in the Sequence Listing and preferably SEQ ID NOs: 1, 3, 5, 7, 9, 10, 12, 14, 16, 18, 20, 22, and 226-233. In the formula, R_2 is oriented so that its 5' end residue is at the left, bound to R_1, and its 3' end residue is at the right, bound to R_3. Any stretch of nucleic acid residues denoted by either R group, where R is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer.

The invention also relates to variants of the polynucleotides described herein that encode for variants of the polypeptides of the invention. Variants that are fragments of the polynucleotides of the invention can be used to synthesize full-length polynucleotides of the

invention. Preferred embodiments are polynucleotides encoding polypeptide variants wherein 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues of a polypeptide sequence of the invention are substituted, added or deleted, in any combination. Particularly preferred are substitutions, additions, and deletions that are silent such that they do not alter the properties

5   or activities of the polynucleotide or polypeptide.

Nucleotide sequences encoding acyltransferases may be obtained from natural sources or be partially or wholly artificially synthesized. They may directly correspond to an acyltransferase endogenous to a natural source or contain modified amino acid sequences, such as sequences which have been mutated, truncated, increased or the like. Acyltransferases

10   may be obtained by a variety of methods, including but not limited to, partial or homogenous purification of protein extracts, protein modeling, nucleic acid probes, antibody preparations and sequence comparisons. Typically an acyltransferase will be derived in whole or in part from a natural source. A natural source includes, but is not limited to, prokaryotic and eukaryotic sources, including, bacteria, yeasts, plants, including algae, and the like.

15   Of special interest are acyltransferases which are obtainable from eukaryotic sources, including those which are obtained, from plants, or from acyltransferases which are obtainable through the use of these sequences. "Obtainable" refers to those acyltransferases which have sufficiently similar sequences to that of the sequences provided herein to provide a biologically active protein of the present invention.

20   Further preferred embodiments of the invention that are at least 50%, 60%, or 70% identical over their entire length to a polynucleotide encoding a polypeptide of the invention, and polynucleotides that are complementary to such polynucleotides. More preferable are polynucleotides that comprise a region that is at least 80% identical over its entire length to a polynucleotide encoding a polypeptide of the invention and polynucleotides that are

25   complementary thereto. In this regard, polynucleotides at least 90% identical over their entire length are particularly preferred, those at least 95% identical are especially preferred. Further, those with at least 97% identity are highly preferred and those with at least 98% and 99% identity are particularly highly preferred, with those at least 99% being the most highly preferred.

30   Preferred embodiments are polynucleotides that encode polypeptides that retain substantially the same biological function or activity as the mature polypeptides encoded by the polynucleotides set forth in the Sequence Listing.

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The invention further relates to polynucleotides that hybridize to the above-described sequences. In particular, the invention relates to polynucleotides that hybridize under stringent conditions to the above-described polynucleotides. As used herein, the terms "stringent conditions" and "stringent hybridization conditions" mean that hybridization will generally occur if there is at least 95% and preferably at least 97% identity between the sequences. An example of stringent hybridization conditions is overnight incubation at 42°C in a solution comprising 50% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/milliliter denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at approximately 65°C. Other hybridization and wash conditions are well known and are exemplified in Sambrook, et al., Molecular Cloning: A Laboratory Manual, Second Edition, cold Spring Harbor, NY (1989), particularly Chapter 11.

The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence set for in the Sequence Listing under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence or a fragment thereof; and isolating said polynucleotide sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers as described herein.

As discussed herein regarding polynucleotide assays of the invention, for example, polynucleotides of the invention can be used as a hybridization probe for RNA, cDNA, or genomic DNA to isolate full length cDNAs or genomic clones encoding a polypeptide and to isolate cDNA or genomic clones of other genes that have a high sequence similarity to a polynucleotide set forth in the Sequence Listing. Such probes will generally comprise at least 15 bases. Preferably such probes will have at least 30 bases and can have at least 50 bases. Particularly preferred probes will have between 30 bases and 50 bases, inclusive.

The coding region of each gene that comprises or is comprised by a polynucleotide sequence set forth in the Sequence Listing may be isolated by screening using a DNA sequence provided in the Sequence Listing to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the invention is then used to screen a library of cDNA, genomic DNA or mRNA to identify members of the library which hybridize to the probe. For example, synthetic oligonucleotides are prepared which correspond to the N-terminal sequence of the polypeptide. The partial sequences so prepared can then be used as probes to obtain acyltransferase clones from a gene library prepared from

a cell source of interest. Alternatively, where oligonucleotides of low degeneracy can be prepared from particular peptides, such probes may be used directly to screen gene libraries for gene sequences. In particular, screening of cDNA libraries in phage vectors is useful in such methods due to lower levels of background hybridization.

Typically, a sequence obtainable from the use of nucleic acid probes will show 60-70% sequence identity between the target acyltransferase sequence and the encoding sequence used as a probe. However, lengthy sequences with as little as 50-60% sequence identity may also be obtained. The nucleic acid probes may be a lengthy fragment of the nucleic acid sequence, or may also be a shorter, oligonucleotide probe. When longer nucleic acid fragments are employed as probes (greater than about 100 bp), one may screen at lower stringencies in order to obtain sequences from the target sample which have 20-50% deviation (i.e., 50-80% sequence homology) from the sequences used as probe. Oligonucleotide probes can be considerably shorter than the entire nucleic acid sequence encoding an acyltransferase enzyme, but should be at least about 10, preferably at least about 15, and more preferably at least about 20 nucleotides. A higher degree of sequence identity is desired when shorter regions are used as opposed to longer regions. It may thus be desirable to identify regions of highly conserved amino acid sequence to design oligonucleotide probes for detecting and recovering other related genes. Shorter probes are often particularly useful for polymerase chain reactions (PCR), especially when highly conserved sequences can be identified. (See, Gould, et al., PNAS USA (1989) 86:1934-1938).

The skilled artisan will appreciate that, in many cases, an isolated cDNA sequence will be incomplete, in that the region coding for the polypeptide is truncated with respect to the 5' terminus of the cDNA. This is a consequence of the reverse transcriptase, an enzyme with low 'processivity' (a measure of the ability of the enzyme to remain attached to the template during the polymerization reaction) employed during the first strand cDNA synthesis.

There are several methods available and are well know to the skilled artisan to obtain full-length cDNAs, or extend short cDNAs, for example those based on the method of Rapid Amplification of cDNA Ends (RACE) (see, for example, Frohman et al. (1988) Proc. Natl. Acad. Sci. USA 85:8998-9002). Recent modifications of the technique, exemplified by the Marathon™ technology (Clonetech Laboratories, Inc.) for example, have significantly simplified obtaining full-length cDNA sequences.

Another aspect of the present invention relates to isolated acyltransferase polypeptides. Such polypeptides include isolated polypeptides set forth in the Sequence Listing, as well as polypeptides and fragments thereof, particularly those polypeptides which exhibit acyltransferase activity and also those polypeptides which have at least 50%, 60% or 70% identity, preferably at least 80% identity, more preferably at least 90% identity, and most preferably at least 95% identity to a polypeptide sequence selected from the group of sequences set forth in the Sequence Listing, and also include portions of such polypeptides, wherein such portion of the polypeptide preferably includes at least 30 amino acids and more preferably includes at least 50 amino acids.

"Identity", as is well understood in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as determined by the match between strings of such sequences. "Identity" can be readily calculated by known methods including, but not limited to, those described in *Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York (1988); *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part I*, Griffin, A.M. and Griffin, H.G., eds., Humana Press, New Jersey (1994); *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press (1987); *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., Stockton Press, New York (1991); and Carillo, H., and Lipman, D., SIAM *J Applied Math*, 48:1073 (1988). Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to determine identity are codified in publicly available programs. Computer programs which can be used to determine identity between two sequences include, but are not limited to, GCG (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); suite of five BLAST programs, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12:* 76-80 (1994); Birren, *et al., Genome Analysis, 1:* 543-559 (1997)). The BLAST X program is publicly available from NCBI and other sources (*BLAST Manual*, Altschul, S., *et al.*, NCBI NLM NIH, Bethesda, MD 20894; Altschul, S., *et al., J. Mol. Biol.*, 215:403-410 (1990)). The well known Smith Waterman algorithm can also be used to determine identity.

Parameters for polypeptide sequence comparison typically include the following:

Algorithm: Needleman and Wunsch, *J. Mol. Biol.* 48:443-453 (1970)

Comparison matrix: BLOSSUM62 from Hentikoff and Hentikoff, *Proc. Natl. Acad. Sci USA* 89:10915-10919 (1992)

Gap Penalty: 12

Gap Length Penalty: 4

A program which can be used with these parameters is publicly available as the "gap" program from Genetics Computer Group, Madison Wisconsin. The above parameters along with no penalty for end gap are the default parameters for peptide comparisons.

Parameters for polynucleotide sequence comparison include the following:

Algorithm: Needleman and Wunsch, J. Mol. Biol. 48:443-453 (1970)

Comparison matrix: matches = +10; mismatches = 0

Gap Penalty: 50

Gap Length Penalty: 3

A program which can be used with these parameters is publicly available as the "gap" program from Genetics Computer Group, Madison Wisconsin. The above parameters are the default parameters for nucleic acid comparisons.

The invention also includes polypeptides of the formula:

$$X-(R_1)_n-(R_2)-(R_3)_n-Y$$
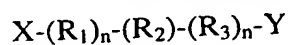
wherein, at the amino terminus, X is hydrogen, and at the carboxyl terminus, Y is hydrogen or a metal, R_1 and R_3 are any amino acid residue, n is an integer between 1 and 1000, and R_2 is an amino acid sequence of the invention, particularly an amino acid sequence selected from the group set forth in the Sequence Listing and preferably SEQ ID NOs: 2, 4, 6, 8, 11, 13, 15, 17, 19, 21, 23, and 218-225. In the formula, R_2 is oriented so that its amino terminal residue is at the left, bound to R_1, and its carboxy terminal residue is at the right, bound to R_3. Any stretch of amino acid residues denoted by either R group, where R is greater than 1, may be either a heteropolymer or a homopolymer, preferably a heteropolymer.

Polypeptides of the present invention include isolated polypeptides encoded by a polynucleotide comprising a sequence selected from the group of a sequence contained in SEQ ID NOs: 1, 3, 5, 7, 9, 10, 12, 14, 16, 18, 20, 22, and 226-233.

The polypeptides of the present invention can be mature protein or can be part of a fusion protein.

Fragments and variants of the polypeptides are also considered to be a part of the invention. A fragment is a variant polypeptide which has an amino acid sequence that is entirely the same as part but not all of the amino acid sequence of the previously described polypeptides. The fragments can be "free-standing" or comprised within a larger polypeptide of which the fragment forms a part or a region, most preferably as a single continuous region. Preferred fragments are biologically active fragments which are those fragments that mediate activities of the polypeptides of the invention, including those with similar activity or improved activity or with a decreased activity. Also included are those fragments that antigenic or immunogenic in an animal, particularly a human.

Variants of the polypeptide also include polypeptides that vary from the sequences set forth in the Sequence Listing by conservative amino acid substitutions, substitution of a residue by another with like characteristics. In general, such substitutions are among Ala, Val, Leu and Ile; between Ser and Thr; between Asp and Glu; between Asn and Gln; between Lys and Arg; or between Phe and Tyr. Particularly preferred are variants in which 5 to 10; 1 to 5; 1 to 3 or one amino acid(s) are substituted, deleted, or added, in any combination.

Variants that are fragments of the polypeptides of the invention can be used to produce the corresponding full length polypeptide by peptide synthesis. Therefore, these variants can be used as intermediates for producing the full-length polypeptides of the invention.

The polynucleotides and polypeptides of the invention can be used, for example, in the transformation of various host cells, as further discussed herein.

The invention also provides polynucleotides that encode a polypeptide that is a mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids within the mature polypeptide (for example, when the mature form of the protein has more than one polypeptide chain). Such sequences can, for example, play a role in the processing of a protein from a precursor to a mature form, allow protein transport, shorten or lengthen protein half-life, or facilitate manipulation of the protein in assays or production. It is contemplated that cellular enzymes can be used to remove any additional amino acids from the mature protein.

A precursor protein, having the mature form of the polypeptide fused to one or more prosequences may be an inactive form of the polypeptide. The inactive precursors generally are activated when the prosequences are removed. Some or all of the prosequences may be removed prior to activation. Such precursor protein are generally called proproteins.

The polynucleotide and polypeptide sequences can also be used to identify additional sequences which are homologous to the sequences of the present invention. The most preferable and convenient method is to store the sequence in a computer readable medium, for example, floppy disk, CD ROM, hard disk drives, external disk drives and DVD, and then

5   to use the stored sequence to search a sequence database with well known searching tools. Examples of public databases include the DNA Database of Japan (DDBJ)(http://www.ddbj.nig.ac.jp/); Genebank (http://www.ncbi.nlm.nih.gov/web/Genbank/Index.html); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL)

10   (http://www.ebi.ac.uk/ebi_docs/embl_db.html). A number of different search algorithms are available to the skilled artisan, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12:* 76-80

15   (1994); Birren, *et al., Genome Analysis, 1:* 543-559 (1997)). Additional programs are available in the art for the analysis of identified sequences, such as sequence alignment programs, programs for the identification of more distantly related sequences, and the like, and are well known to the skilled artisan.

20   **Plant Constructs and Methods of Use**

Of interest in the present invention, is the use of the nucleotide sequences, or polynucleotides, in recombinant DNA constructs to direct the transcription or transcription and translation (expression) of the acyltransferase sequences of the present invention in a host

25   cell.

Of particular interest is the use of the nucleotide sequences, or polynucleotides, in recombinant DNA constructs to direct the transcription or transcription and translation (expression) of the acyltransferase sequences of the present invention in a host cell. The expression constructs generally comprise a promoter functional in a host cell operably linked

30   to a nucleic acid sequence encoding an acyltransferase of the present invention and a transcriptional termination region functional in a host cell.

By "host cell" is meant a cell which contains a vector and supports the replication, and/or transcription or transcription and translation (expression) of the expression construct.

Host cells for use in the present invention can be prokaryotic cells, such as *E. coli*, or eukaryotic cells such as yeast, plant, insect, amphibian, or mammalian cells. Preferably, host cells are monocotyledenous or dicotyledenous plant cells.

Of particular interest in the present invention is the use of the polynucleotides of the present invention for the preparation of constructs to direct the transcription or transcription and translation of the nucleotide sequences encoding an acyltransferase in a host plant cell. Plant expression constructs generally comprise a promoter functional in a plant host cell operably linked to a nucleic acid sequence of the present and a transcriptional termination region functional in a host plant cell.

Those skilled in the art will recognize that there are a number of promoters which are functional in plant cells, and have been described in the literature. Chloroplast and plastid specific promoters, chloroplast or plastid functional promoters, and chloroplast or plastid operable promoters are also envisioned.

One set of promoters are constitutive promoters such as the CaMV35S or FMV35S promoters that yield high levels of expression in most plant organs. Enhanced or duplicated versions of the CaMV35S and FMV35S promoters are useful in the practice of this invention (Odell, *et al.* (1985) *Nature* 313:810-812; Rogers, U.S. Patent Number 5,378, 619). In addition, it may also be preferred to bring about expression of the protein of interest in specific tissues of the plant, such as leaf, stem, root, tuber, seed, fruit, etc., and the promoter chosen should have the desired tissue and developmental specificity.

Of particular interest is the expression of the nucleic acid sequences of the present invention from transcription initiation regions which are preferentially expressed in a plant seed tissue. Examples of such seed preferential transcription initiation sequences include those sequences derived from sequences encoding plant storage protein genes or from genes involved in fatty acid biosynthesis in oilseeds. Examples of such promoters include the 5' regulatory regions from such genes as napin (Kridl *et al.*, *Seed Sci. Res. 1*:209:219 (1991)), phaseolin, zein, soybean trypsin inhibitor, ACP, stearoyl-ACP desaturase, soybean α' subunit of β-conglycinin (soy 7s, (Chen *et al.*, *Proc. Natl. Acad. Sci.*, 83:8560-8564 (1986))) and oleosin.

It may be advantageous to direct the localization of proteins conferring acyltransferase to a particular subcellular compartment, for example, to the mitochondrion, endoplasmic reticulum, vacuoles, chloroplast or other plastidic compartment. For example, where the genes of interest of the present invention will be targeted to plastids, such as chloroplasts, for

expression, the constructs will also employ the use of sequences to direct the gene to the plastid. Such sequences are referred to herein as chloroplast transit peptides (CTP) or plastid transit peptides (PTP). In this manner, where the gene of interest is not directly inserted into the plastid, the expression construct will additionally contain a gene encoding a transit

5   peptide to direct the gene of interest to the plastid. The chloroplast transit peptides may be derived from the gene of interest, or may be derived from a heterologous sequence having a CTP. Such transit peptides are known in the art. See, for example, Von Heijne *et al.* (1991) *Plant Mol. Biol. Rep. 9*:104-126; Clark *et al.* (1989) *J. Biol. Chem. 264*:17544-17550; della-Cioppa *et al.* (1987) *Plant Physiol. 84*:965-968; Romer *et al.* (1993) *Biochem. Biophys. Res*

10   *Commun. 196*:1414-1421; and, Shah *et al.* (1986) *Science 233*:478-481. Additional transit peptides for the translocation of the protein to the endoplasmic reticulum (ER), or vacuole may also find use in the constructs of the present invention.

Depending upon the intended use, the constructs may contain the nucleic acid sequence which encodes the entire acyltransferase protein, or a portion thereof. For example,

15   where antisense inhibition of a given acyltransferase protein is desired, the entire sequence is not required. Furthermore, where acyltransferase sequences used in constructs are intended for use as probes, it may be advantageous to prepare constructs containing only a particular portion of a acyltransferase encoding sequence, for example a sequence which is discovered to encode a highly conserved acyltransferase region.

20   The skilled artisan will recognize that there are various methods for the inhibition of expression of endogenous sequences in a host cell. Such methods include, but are not limited to antisense suppression (Smith, *et al.* (1988) *Nature* 334:724-726) , co-suppression (Napoli, *et al.* (1989) *Plant Cell* 2:279-289), ribozymes (PCT Publication WO 97/10328), and combinations of sense and antisense, such as those described by Waterhouse, *et al.* (1998)

25   *Proc. Natl. Acad. Sci. USA* 95:13959-13964. Methods for the suppression of endogenous sequences in a host cell typically employ the transcription or transcription and translation of at least a portion of the sequence to be suppressed. Such sequences may be homologous to coding as well as non-coding regions of the endogenous sequence.

Regulatory transcript termination regions may be provided in plant expression

30   constructs of this invention as well. Transcript termination regions may be provided by the DNA sequence encoding the acyltransferase or a convenient transcription termination region derived from a different gene source, for example, the transcript termination region which is naturally associated with the transcript initiation region. The skilled artisan will recognize

that any convenient transcript termination region which is capable of terminating transcription in a plant cell may be employed in the constructs of the present invention.

Alternatively, constructs may be prepared to direct the expression of the acyltransferase sequences directly from the host plant cell plastid. Such constructs and

5   methods are known in the art and are generally described, for example, in Svab, *et al.* (1990) *Proc. Natl. Acad. Sci. USA* 87:8526-8530 and Svab and Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90:913-917 and in U.S. Patent Number 5,693,507.

A plant cell, tissue, organ, or plant into which the recombinant DNA constructs containing the expression constructs have been introduced is considered transformed,

10 transfected, or transgenic. A transgenic or transformed cell or plant also includes progeny of the cell or plant and progeny produced from a breeding program employing such a transgenic plant as a parent in a cross and exhibiting an altered genotype resulting from the presence of an introduced acyltransferase nucleic acid sequence.

The term "introduced" in the context of inserting a nucleic acid sequence into a cell,

15 means "transfection", or "transformation" or "transduction" and includes reference to the incorporation of a nucleic acid sequence into a eukaryotic or prokaryotic cell where the nucleic acid sequence may be incorporated into the genome of the cell (for example, chromosome, plasmid, plastid, or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (for example, transfected mRNA).

20 Plant expression or transcription constructs having an acyltransferase as the DNA sequence of interest for increased or decreased expression thereof may be employed with a wide variety of plant life, particularly, plant life involved in the production of vegetable oils for edible and industrial uses. Plants of interest in the present invention include monocotyledenous and dicotyledenous plants. Most especially preferred are temperate

25 oilseed crops. Plants of interest include, but are not limited to, rapeseed (Canola and High Erucic Acid varieties), sunflower, safflower, cotton, soybean, peanut, coconut and oil palms, and corn. Depending on the method for introducing the recombinant constructs into the host cell, other DNA sequences may be required. Importantly, this invention is applicable to dicotyledyons and monocotyledons species alike and will be readily applicable to new and/or

30 improved transformation and regulation techniques.

As used herein, the term "plant" includes reference to whole plants, plant organs (for example, leaves, stems, roots, etc.), seeds, and plant cells and progeny of same. Plant cell, as used herein includes, without limitation, seeds suspension cultures, embryos, meristematic

regions, callus tissue, leaves roots shoots, gametophytes, sporophytes, pollen, and microspores. The class of plants which can be used in the methods of the present invention is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledenous and dicotyledenous plants. Particularly preferred plants of

5   interest include, but are not limited to, rapeseed (Canola and High Erucic Acid varieties), sunflower, safflower, cotton, soybean, peanut, coconut and oil palms, and corn. Most especially preferred plants include *Brassica*, soybean, and corn.

As used herein, "transgenic plant" includes reference to a plant which comprises within its genome a heterologous polynucleotide. Generally, the heterologous polynucleotide

10   is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acid including those transgenics initially so altered as well

15   as those created by sexual crosses or asexual propagation from the initial transgenic.

Thus a plant having within its cells a heterologous polynucleotide is referred to herein as a transgenic plant. The heterologous polynucleotide can be either stably integrated into the genome, or can be extra-chromosomal. Preferably, the polynucleotide of the present invention is stably integrated into the genome such that the polynucleotide is passed on to

20   successive generations. The polynucleotide is integrated into the genome alone or as part of a recombinant expression cassette. "Transgenic" is used herein to include any cell, cell line, callus, tissue, plant part or plant, the genotype of which has been altered by the presence of heterologous nucleic acids including those transgenics initially so altered as well as those created by sexual crosses or asexual reproduction of the initial transgenics.

25   As used herein, "heterologous" in reference to a nucleic acid is a nucleic acid that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. For example, a promoter operably linked to a heterologous structural gene is from a species different from that from which the structural gene was derived, or, if from the same species,

30   one or both are substantially modified from their original form. A heterologous protein may originate from a foreign species, or, if from the same species, is substantially modified from its original form by deliberate human intervention.

As used herein, a "recombinant expression cassette" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements which permit transcription of a particular nucleic acid in a target cell. The recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Typically, the recombinant expression cassette portion of an expression vector includes, among other sequences, a nucleic acid sequence to be transcribed and a promoter.

It is contemplated that the gene sequences may be synthesized, either completely or in part, especially where it is desirable to provide plant-preferred sequences. Thus, all or a portion of the desired structural gene (that portion of the gene which encodes the acyltransferase protein) may be synthesized using codons preferred by a selected host. Host-preferred codons may be determined, for example, from the codons used most frequently in the proteins expressed in a desired host species.

One skilled in the art will readily recognize that antibody preparations, nucleic acid probes (DNA and RNA) and the like may be prepared and used to screen and recover "homologous" or "related" acyltransferase from a variety of plant sources. Homologous sequences are found when there is an identity of sequence, which may be determined upon comparison of sequence information, nucleic acid or amino acid, or through hybridization reactions between a known acyltransferase and a candidate source. Conservative changes, such as Glu/Asp, Val/Ile, Ser/Thr, Arg/Lys and Gln/Asn may also be considered in determining sequence homology. Amino acid sequences are considered homologous by as little as 25% sequence identity between the two complete mature proteins. (*See* generally, Doolittle, R.F., *OF URFS and ORFS* (University Science Books, CA, 1986.)

Thus, other acyltransferase sequences can be obtained from the specific exemplified sequences provided herein. Furthermore, it will be apparent that one can obtain natural and synthetic sequences, including modified amino acid sequences and starting materials for synthetic-protein modeling from the exemplified sequences and from acyltransferases which are obtained through the use of such exemplified sequences. Modified amino acid sequences include sequences which have been mutated, truncated, increased and the like, whether such sequences were partially or wholly synthesized. Sequences which are actually purified from plant preparations or are identical or encode identical proteins thereto, regardless of the method used to obtain the protein or sequence, are equally considered naturally derived.

For immunological screening, antibodies to the acyltransferase protein can be prepared by injecting rabbits or mice with the purified protein or portion thereof, such methods of preparing antibodies being well known to those in the art. Either monoclonal or polyclonal antibodies can be produced, although typically polyclonal antibodies are more useful for gene isolation. Western analysis may be conducted to determine that a related protein is present in a crude extract of the desired plant species, as determined by cross-reaction with the antibodies to the acyltransferase protein. When cross-reactivity is observed, genes encoding the related proteins are isolated by screening expression libraries representing the desired plant species. Expression libraries can be constructed in a variety of commercially available vectors, including lambda gt11, as described in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory, Cold Spring Harbor, New York).

The nucleic acid sequences associated with acyltransferase proteins will find many uses. For example, recombinant constructs can be prepared which can be used as probes, or which will provide for expression of the acyltransferase protein in host cells to produce a ready source of the enzyme and/or to modify the composition of triglycerides found therein. Other useful applications may be found when the host cell is a plant host cell, either *in vitro* or *in vivo*.

The modification of fatty acid compositions may also affect the fluidity of plant membranes. Different lipid concentrations have been observed in cold-hardened plants, for example. By this invention, one may be capable of introducing traits which will lend to chill tolerance. Constitutive or temperature inducible transcription initiation regulatory control regions may have special applications for such uses.

As discussed above, nucleic acid sequence encoding an acyltransferase of this invention may include genomic, cDNA or mRNA sequence. By "encoding" is meant that the sequence corresponds to a particular amino acid sequence either in a sense or anti-sense orientation. By "extrachromosomal" is meant that the sequence is outside of the plant genome of which it is naturally associated. By "recombinant" is meant that the sequence contains a genetically engineered modification through manipulation via mutagenesis, restriction enzymes, and the like.

Once the desired acyltransferase nucleic acid sequence is obtained, it may be manipulated in a variety of ways. Where the sequence involves non-coding flanking regions, the flanking regions may be subjected to resection, mutagenesis, etc. Thus, transitions,

transversions, deletions, and insertions may be performed on the naturally occurring sequence. In addition, all or part of the sequence may be synthesized. In the structural gene, one or more codons may be modified to provide for a modified amino acid sequence, or one or more codon mutations may be introduced to provide for a convenient restriction site or

5   other purpose involved with construction or expression. The structural gene may be further modified by employing synthetic adapters, linkers to introduce one or more convenient restriction sites, or the like.

The nucleic acid or amino acid sequences encoding an acyltransferase of this invention may be combined with other non-native, or "heterologous", sequences in a variety

10   of ways. By "heterologous" sequences is meant any sequence which is not naturally found joined to the acyltransferase, including, for example, combinations of nucleic acid sequences from the same plant which are not naturally found joined together.

The DNA sequence encoding an acyltransferase of this invention may be employed in conjunction with all or part of the gene sequences normally associated with the

15   acyltransferase. In its component parts, a DNA sequence encoding acyltransferase is combined in a DNA construct having, in the 5' to 3' direction of transcription, a transcription initiation control region capable of promoting transcription and translation in a host cell, the DNA sequence encoding plant acyltransferase and a transcription and translation termination region.

20   Potential host cells include both prokaryotic cells, such as *E.coli* and eukaryotic cells such as yeast, insect, amphibian, or mammalian cells. A host cell may be unicellular or found in a multicellular differentiated or undifferentiated organism depending upon the intended use. Preferably, host cells of the present invention include plant cells, both monocotyledenous and dicotyledenous. Cells of this invention may be distinguished by

25   having a sequence foreign to the wild-type cell present therein, for example, by having a recombinant nucleic acid construct encoding an acyltransferase therein.

The methods used for the transformation of the host plant cell are not critical to the present invention. The transformation of the plant is preferably permanent, i.e. by integration of the introduced expression constructs into the host plant genome, so that the introduced

30   constructs are passed onto successive plant generations. The skilled artisan will recognize that a wide variety of transformation techniques exist in the art, and new techniques are continually becoming available. Any technique that is suitable for the target host plant can be employed within the scope of the present invention. For example, the constructs can be

introduced in a variety of forms including, but not limited to as a strand of DNA, in a plasmid, or in an artificial chromosome. The introduction of the constructs into the target plant cells can be accomplished by a variety of techniques, including, but not limited to calcium-phosphate-DNA co-precipitation, electroporation, microinjection, *Agrobacterium*

5 infection, liposomes or microprojectile transformation. The skilled artisan can refer to the literature for details and select suitable techniques for use in the methods of the present invention.

Normally, included with the DNA construct will be a structural gene having the necessary regulatory regions for expression in a host and providing for selection of

10 transformant cells. The gene may provide for resistance to a cytotoxic agent, e.g. antibiotic, heavy metal, toxin, etc., complementation providing prototrophy to an auxotrophic host, viral immunity or the like. Depending upon the number of different host species the expression construct or components thereof are introduced, one or more markers may be employed, where different conditions for selection are used for the different hosts.

15 Where *Agrobacterium* is used for plant cell transformation, a vector may be used which may be introduced into the *Agrobacterium* host for homologous recombination with T-DNA or the Ti- or Ri-plasmid present in the *Agrobacterium* host. The Ti- or Ri-plasmid containing the T-DNA for recombination may be armed (capable of causing gall formation) or disarmed (incapable of causing gall formation), the latter being permissible, so long as the

20 *vir* genes are present in the transformed *Agrobacterium* host. The armed plasmid can give a mixture of normal plant cells and gall.

In some instances where *Agrobacterium* is used as the vehicle for transforming host plant cells, the expression or transcription construct bordered by the T-DNA border region(s) will be inserted into a broad host range vector capable of replication in *E. coli* and

25 *Agrobacterium*, there being broad host range vectors described in the literature. Commonly used is pRK2 or derivatives thereof. See, for example, Ditta, *et al.*, *(Proc. Nat. Acad. Sci., U.S.A.* (1980) *77*:7347-7351) and EPA 0 120 515, which are incorporated herein by reference. Alternatively, one may insert the sequences to be expressed in plant cells into a vector containing separate replication sequences, one of which stabilizes the vector in *E. coli*, and

30 the other in *Agrobacterium*. See, for example, McBride and Summerfelt *(Plant Mol. Biol.* (1990) *14*:269-276), wherein the pRiHRI (Jouanin, *et al., Mol. Gen. Genet.* (1985) 201:370-374) origin of replication is utilized and provides for added stability of the plant expression vectors in host *Agrobacterium* cells.

Included with the expression construct and the T-DNA will be one or more markers, which allow for selection of transformed Agrobacterium and transformed plant cells. A number of markers have been developed for use with plant cells, such as resistance to chloramphenicol, kanamycin, the aminoglycoside G418, hygromycin, or the like. The particular marker employed is not essential to this invention, one or another marker being preferred depending on the particular host and the manner of construction.

For transformation of plant cells using *Agrobacterium*, explants may be combined and incubated with the transformed *Agrobacterium* for sufficient time for transformation, the bacteria killed, and the plant cells cultured in an appropriate selective medium. Once callus forms, shoot formation can be encouraged by employing the appropriate plant hormones in accordance with known methods and the shoots transferred to rooting medium for regeneration of plants. The plants may then be grown to seed and the seed used to establish repetitive generations and for isolation of vegetable oils.

There are several possible ways to obtain the plant cells of this invention which contain multiple expression constructs. Any means for producing a plant comprising a construct having a nucleic acid sequence of the present invention, and at least one other construct having another DNA sequence encoding an enzyme are encompassed by the present invention. For example, the expression construct can be used to transform a plant at the same time as the second construct either by inclusion of both expression constructs in a single transformation vector or by using separate vectors, each of which express desired genes. The second construct can be introduced into a plant which has already been transformed with the first expression construct, or alternatively, transformed plants, one having the first construct and one having the second construct, can be crossed to bring the constructs together in the same plant.

In general, acyltransferase proteins are active in the transfer of acyl groups from a donor to a variety of different substrates. For example, diacylglycerol acyltransferases add acyl groups to diacylglycerol to form triacylglycerol (TAG), oracyl:CoA:cholesterol acyltransferase uses an acyl-CoA as a donor to transfer an acyl group to a sterol to form a sterol ester. Typically, the substrates include, but are not limited to glycerides, including mono and diglycerides, sterols, stanols, phosphatides, and the like. Donors include, but are not limited to acyl-CoA and acyl-ACP molecules.

The invention now being generally described, it will be more readily understood by reference to the following examples which are included for purposes of illustration only and are not intended to limit the present invention.

EXAMPLES

Example 1: RNA Isolations

Total RNA from the inflorescence and developing seeds of *Arabidopsis thaliana* is isolated for use in construction of complementary (cDNA) libraries. The procedure is an adaptation of the DNA isolation protocol of Webb and Knapp (D.M. Webb and S.J. Knapp, (1990) Plant Molec. Reporter, 8, 180-185). The following description assumes the use of 1g fresh weight of tissue. Frozen seed tissue is powdered by grinding under liquid nitrogen. The powder is added to 10ml REC buffer (50mM Tris-HCl, pH 9, 0.8M NaCl, 10mM EDTA, 0.5% w/v CTAB (cetyltrimethyl-ammonium bromide)) along with 0.2g insoluble polyvinylpolypyrrolidone, and ground at room temperature. The homogenate is centrifuged for 5 minutes at 12,000 x*g* to pellet insoluble material. The resulting supernatant fraction is extracted with chloroform, and the top phase is recovered.

The RNA is then precipitated by addition of 1 volume RecP (50mM Tris-HCL pH9, 10mM EDTA and 0.5% (w/v) CTAB) and collected by brief centrifugation as before. The RNA pellet is redissolved in 0.4 ml of 1M NaCl. The RNA pellet is redissolved in water and extracted with phenol/chloroform. Sufficient 3M potassium acetate (pH 5) is added to make the mixture 0.3M in acetate, followed by addition of two volumes of ethanol to precipitate the RNA. After washing with ethanol, this final RNA precipitate is dissolved in water and stored frozen.

Alternatively, total RNA may be obtained using TRIzol reagent (BRL-Lifetechnologies, Gaithersburg, MD) following the manufacturers protocol. The RNA precipitate is dissolved in water and stored frozen.

Example 2: Identification of Acyltransferase Homology Sequences

Searches are performed on a Silicon Graphics Unix computer using additional Bioaccellerator hardware and GenWeb software supplied by Compugen Ltd. This software and hardware enables the use of the Smith-Waterman algorithm in searching DNA and
5 protein databases using profiles as queries. The program used to query protein databases is profilesearch. This is a search where the query is not a single sequence but a profile based on a multiple alignment of amino acid or nucleic acid sequences. The profile is used to query a sequence data set, i.e., a sequence database. The profile contains all the pertinent information for scoring each position in a sequence, in effect replacing the "scoring matrix" used for the
10 standard query searches. The program used to query nucleotide databases with a protein profile is tprofilesearch. Tprofilesearch searches nucleic acid databases using an amino acid profile query. As the search is running, sequences in the database are translated to amino acid sequences in six reading frames. The output file for tprofilesearch is identical to the output file for profilesearch except for an additional column that indicates the frame in which the
15 best alignment occurred.

The Smith-Waterman algorithm, (Smith and Waterman (1981) *supra*), is used to search for similarities between one sequence from the query and a group of sequences contained in the database. E score values as well as other sequence information, such as conserved peptide sequences of HXXXXD and PEG are used to identify related sequences.
20 By using the conserved peptide sequence information, E score values of greater than E-12 and E-8 are considered. For example, the EST sequence originally used to identify ATAT2 had an E score of 0.0094, while the EST sequence originally used to identify ATLPAAT1 had an E score of 0.0868.

A protein sequence of glycerol-3-phosphate from *E. coli* (Swiss Prot Accession
25 P00482) is used to search the NCBI non-redundant protein database using BLAST. In the first round of searches, other membrane forms of G3PAAT are identified. In subsequent PSI-BLAST searches (Altschul, *et al.* (1997) *Nucleic Acids Res* 25:3389-3402), LPAATs and other acyltransferases are identified. Using sequence alignment software programs, G3PAAT and different LPAAT amino acid sequences are aligned, and a profile is generated using a
30 homologous sequence region, between amino acids 256 and 459 of the *E. coli* sequence.

The identified 204 amino acid is used to query the protein database using PSI-BLAST. After 5 iterations of PSI-BLAST, the profile generated from this new query (Figure 1)

identified soluble forms of G3PAAT. Prior to this identification, no sequence homology had been identified between the membrane and soluble forms of G3PAAT.

5   **Example 3:** Excision of PSI-BLAST Profile

The profile generated from the queries using PSI-BLAST is excised from the hyper text markup language (html) file. The worldwide web (www)/html interface to psiblast at ncbi stores the current generated profile matrix in a hidden field in the html file that is

10   returned after each iteration of psiblast. However, this matrix has been encoded into string62 (s62) format for ease of transport through html. String62 format is a simple conversion of the values of the matrix into html legal ascii characters.

The encoded matrix width (x axis) is 26 characters, and comprise the consensus characters, the probabilities of each amino acid in the order A,B,C,D,E,F,G,H,I,K,L,M,N,

15   P,Q,R,S,T,V,W,X,Y,Z (where B represents D and N, and Z represents Q and E, and X represents any amino acid), gap creation value, and gap extension value.

The length (y axis) of the matrix corresponds to the length of the sequences identified by PSI-BLAST. The order of the amino acids corresponds to the conserved amino acid sequence of the sequences identified using PSI-BLAST, with the N-terminal end at the top of

20   the matrix. The probabilities of other amino acids at that position are represented for each amino acid along the x axis, below the respective single letter amino acid abbreviation.

Thus, each row of the profile consists of the highest scoring (consensus) amino acid, followed by the scores for each possible amino acid at that position in sequence matrix, the score for opening a gap that that position, and the score for continuing a gap at that position.

25   The string62 file is converted back into a profile for use in subsequent searches. The gap open field is set to 11 and the gap extension field is set to 1 along the x axis. The gap creation and gap extension values are known, based on the settings given to the PSI-BLAST algorithm. The matrix is exported to the standard GCG profile form. This format can be read by GenWeb.

30   The algorithm used to convert the string62 formatted file to the matrix is outlined in Table 1.

Table 1

1. if encoded character z then the value is blast score min
2. if encoded character Z then the value is blast score max
3. else if the encoded character is uppercase then its value is (64-(ascii # of char))
4. else if the encoded character is a digit the value is ((ascii # of char)-48)
5. else if the encoded character is not uppercase then the value is ((ascii # of char) - 87)
6. ALL B positions are set to min of D and N amino acids at that row in sequence matrix
7. ALL Z positions are set to min of Q amd E amino acids at that row in sequence matrix
8. ALL X positions are set to min of all amino acids at that row in sequence matrix
9. kBLAST_SCORE_MAX=999;
10. kBLAST_SCORE_MIN=-999;
11. all gap opens are set to 11
12. all gap lens are set to 1

Example 4: Identification of Novel Acyltransferase Related Amino Acid Sequences

The profile (Figure 1) is used in further queries to identify a number of previously unidentified proteins from yeast as novel acyltransferases. A protein is identified from an *Arabidopsis* protein sequence database (ATAT1) (SEQ ID NO:2). Sequences are also identified from nucleic acid databases (Table 2)

Table 2

Database ID Number	BLAST Search Hits	Log probability
Saccharomyces cerevisiae		
gi 1078509 NO:217)	Limnanthes putative LPAAT	e-10 (SEQ ID
gi 586485 NO:218)	Limnanthes putative LPAAT	e-13 (SEQ ID

gi 320748 NO:219)	Limnanthes putative LPAAT	e-19 (SEQ ID
gi 2506920		SUPPRESSES CTR1 (choline transport mutant) (SEQ ID NO:220)
gi 549627 NO:221)	similar to CTR1	e-118 (SEQ ID
gi 2133031 NO:222)	unidentified	(SEQ ID
gi 2132939 NO:223)	unidentified	(SEQ ID
gi 2132299 NO:224)	TAFAZZIN	e-14 (SEQ ID

In Table 2, the gi number is the database identifier, the middle column shows the results of BLAST searches against the NCBI NR protein database, and the log probability number shows represents the log of the probability of such a match occurring by random chance. These proteins, including the ATAT1 protein sequence, are identified using the original PSI-BLAST search of the NCBI NR protein database. Thus, these proteins are novel acyltransferase related proteins with unidentified activities.

The *Arabidopsis* acyltransferase sequence, herein referred to as ATAT1, is also identified using the original PSI-BLAST search of the NCBI NR protein database, and did not have an annotated function.

Additional *Arabidopsis* amino acid sequences related to acyltransferases are identified from the databases, referred to as ATAT2est, ATAT3est, ATAT4est, ATAT5est, ATAT6est, ATAT7est, ATAT8est, ATAT9, ATAT10, and ATAT11est. Furthermore, *Arabidopsis* amino acid sequences are identified which demonstrate sequence similarity to known lysophosphatidic acid, referred to as ATLPAAT1. The sequences of ATAT9 and ATAT10 are identified from the database as genomic sequences, all other *Arabidopsis* sequences are identified as ESTs.

Example 5: Sequence Analysis of the Novel Acyltransferases

To obtain the entire coding region corresponding to the *Arabidopsis* acyltransferase sequences, synthetic oligo-nucleotide primers are designed to amplify ⋯ 5' ⋯ ' 3' ends o⋯ partial cDNA clones containing ⋯ ⋯ ⋯ ⋯ ⋯ gned ⋯ rding to the ⋯ ⋯ ⋯ ⋯ ⋯ ⋯ ated sequences (Table 3) and used in Rapid Amplification of cDNA Ends (RACE) reactions (Frohman *et al.* (1988) *Proc. Natl Acad. Sci. USA* 85:8998-9002) using the Marathon cDNA amplification kit (Clontech Laboratories Inc, Palo Alto, CA). Primers with an R designation are used for 5' RACE reactions, and primers with an F designation are used for 3' RACE reactions.

Table 3

ATAT2

ATAT2R1   CCATCCGCTTCAAGGGAACGACACCCATCA   (SEQ ID NO:135)

ATAT2R2   TCCCTGTCTTGCTTGATGAACTTAAAGCTTG   (SEQ ID NO:136)

ATAT2R3   ACAGCAGGAGTGTCTGATGATGGCAGATTC   (SEQ ID NO:137)

ATAT3

ATAT3R1   ACTGGAGTTCCAGCCAAAAATGCACCTGTC (SEQ ID NO:138)

ATAT3R2   GATACACCCTTGAAATCAGGCGATTTTGCT   (SEQ ID NO:139)

ATAT4

ATAT4R1   TTGCAAATTCAATTCCTGTTTCACCGGGCC   (SEQ ID NO:140)

ATAT4R2   GTTTTCTGCTATTCCAGAAGGCGTCAACAA   (SEQ ID NO:141)

ATAT5

ATAT5R1   CATTGAAGATCCGTCCGTGAAGTTNCCTTACC (SEQ ID NO:142)

ATAT5R2   TCGAGCTGTGATCGATGATTGGCTGTGAAG   (SEQ ID NO:143)

ATAT5F1   GTCTCTTCAAAAACACACACACGTCTCT   (SEQ ID NO:144)

ATAT5F2   GTCTCTTCAAAAACACACACACGTCTCT   (SEQ ID NO:145)

ATAT6

H76348-F1   GTAGAGAGCCTTACTTGCTTCGGTTTAGTC   (SEQ ID NO:146)

H76348-F2   ACGTCATCGTACCTGTTGCTATTGACTCAC   (SEQ ID NO:147)

H76348-R1   ACTTTTCCATTGTCAGGGACTCCTCGACAC   (SEQ ID NO:148)

H76348-R2   ACGGTGTAGGAAGGGAAAGGATTCAAAAGG (SEQ ID NO:149)

ATAT7

ATTS0193-F1   GCGATGAACTACAGAGTCGGATTCTTCCTC (SEQ ID NO:150)

ATTS0193-F2   CCGGTTTACGAGATTACGTTCTTGAACCAG (SEQ ID NO:151)

ATTS0193-R1   CAATGGAGACAAGGCTCGAAAGTGCTAACC (SEQ ID NO:152)

ATTS0193-R2   ATTCTCTGAACATAGTTCGCCACGGTCATG (SEQ ID NO:153)

ATAT8

AA042618-F1 GAAATCCAACGCCTTCCCAATATCACTCTG (SEQ ID NO:154)

AA042618-F2 CTTCAACTTTCCATCAGGATCTTGGCACGT (SEQ ID NO:155)

AA042618-R1 ACCACTTGTTAGAGACCTTACCTGCTTAGG (SEQ ID NO:156)

AA042618-R2 TCCTACCTACACCATCCAATTTCTCGACCC (SEQ ID NO:157)

ATAT11

ATAT11R1 CTGCGTCAAGTGAGCAACTCAGTTCTTGCA (SEQ ID NO:158)

ATAT11R2 TGGGAAGCAGCACGTTGTTCAGTATCGGAA (SEQ ID NO:159)

ATAT11R3 TAGCCTCTGTGTAATCTGTGCCCTCGGGGA (SEQ ID NO:160)

From the nucleic acid sequences obtained from the RACE reactions, protein sequence is predicted for each nucleic acid sequence using Macvector software. Nucleic acid sequences are provided for ATAT1 (SEQ ID NO:1), ATAT2 (SEQ ID NO:3), ATAT3 (SEQ ID NO:5), ATAT4 (SEQ ID NO:7), ATAT5 (SEQ ID NO:9), ATAT6 (SEQ ID NO:10), ATAT7 (SEQ ID NO:12), ATAT8 (SEQ ID NO:14), ATAT9 (SEQ ID NO:16), ATAT10 (SEQ ID NO:18), ATAT11 (SEQ ID NO:20) and ATLPAAT1 (SEQ ID NO:22), respectively.

The protein sequence derived from the ATAT1 (SEQ ID NO:2) nucleic acid sequence from Arabidopsis has a predicted molecular mass of 32.5 kDa, and a PI of 9.74. Alignment of the Arabidopsis acyltransferase with several LPAAT and G3PAAT shows that some of the domains that are conserved between LPAAT and G3PAAT are conserved in the new acyltransferase protein.

The ATAT2 nucleic acid sequence is predicted to encode a 312 amino acid protein (SEQ ID NO:4), with a molecular weight of 34.6 kD, and a pI of 9.99. The ATAT2 protein may also contain 2 to 3 transmembrane domains. However, the protein encoded by the ATAT2 nucleic acid sequence may be longer than predicted because of the absence of an inframe stop codon upstream of the ATG start codon used.

The ATAT3 nucleic acid sequence is predicted to encode a 398 amino acid protein (SEQ ID NO:6), with a molecular weight of 44.7 kD, and a pI of 5.62. The ATAT3 protein may contain 1 to 4 transmembrane domains. The ATAT4 nucleic acid sequence is predicted to encode a 317 amino acid protein (SEQ ID NO:8), with a molecular weight of 36.5 kD, and a pI of 9.67. The ATAT4 protein is predicted to have 2 to 5 transmembrane domains.

The ATLPAAT1 nucleic acid sequence is predicted to encode a 389 amino acid protein (SEQ ID NO:23), with a molecular weight of 43.7 kD, and a pI of 9.52. The ATLPAAT1 protein is predicted to have up to 3 transmembrane domains. The protein predicted from the ATLPAAT1 nucleic acid sequence is similar to LPAATs reported for

5 *Brassica,* maize, and meadowfoam (described in PCT Publication WO 94/13814). The ATAT11 nucleic acid sequence is predicted to encode a 375 amino acid protein (SEQ ID NO:21), with a molecular weight of 43.5 kD, and a pI of 9.45. The deduced amino acid sequences of ATAT6 (SEQ ID NO:11), ATAT7 (SEQ ID NO:13), ATAT8 (SEQ ID NO:15), ATAT9 (SEQ ID NO:17), and ATAT10 (SEQ ID NO:19) are also provided

10 A sequence region approximately 30 amino acids upstream through approximately 100 amino acids downstream of the conserved amino acid sequences HXXXXD (Heath and Rock, (1998) *J. Bacteriol.* 180(6):1425-1430) and PEG (Neuwald (1997) *Curr Biol* 7:R465-R466) of the predicted amino acid sequences derived from the nucleic acid sequences of ATAT1, ATAT2, ATAT3, ATAT4, ATAT6, ATAT7, ATAT8, ATAT9, ATAT10,

15 ATLPAAT1, and ATAT11 are compared to the amino acid sequences of lysophosphatidic acid acyltransferase (Jojoba AT (SEQ ID NO:162, the nucleic acid sequence is provided in SEQ ID NO:161), maize AT (PCT Publication WO 94/13814), PLSC coco(GenBank accession 1098605), PLSC Lim(GenBank accession 1209507), PLSC, Ecoli (GenBank accession 1209507), and PLSC Yeast(GenBank accession 464422)) and glycerol-3-phosphate

20 acyltransferase (PLSB Ecoli(GenBank accession 130326) and PLSB Mouse(GenBank accession 2498786)) (Figure 2), and similarities are identified (Figure 2 and Figure 3).

Sequence comparisons reveal several classes of acyltransferases exist based on conserved amino acid sequences identified in the comparisons in Figure 2. For example, ATAT1, ATAT6, ATAT7, ATAT8, and ATAT9, contain the conserved amino acid

25 sequences of VTYSXS(SEQ ID NO: 128), VXLTRXR(SEQ ID NO: 129), LXXGDLV(SEQ ID NO: 132) between the HXXXXD and PEG sequences. In addition, ATAT1, ATAT6, ATAT7, ATAT8, and ATAT9 also contain the conserved sequences CPEGT(SEQ ID NO: 130) which comprises the PEG sequence, as well as IVPVA(SEQ ID NO: 131) and VANXXQ (SEQ ID NO: 134)(Figure 2) downstream of the PEG sequence. The sequences

30 corresponding to ATAT1, ATAT7, and ATAT9 are the most closely related in this class, with similarities between ATAT1 and ATAT9 of 67.0%, between ATAT1 and ATAT7 of 58.2% and between ATAT9 and ATAT7 of 63.9% (Figure 3B).

Sequence comparisons also demonstrate that the sequence of ATLPAAT1 is most closely related to the jojoba LPAAT (82.3% similar), and maize (78.0% similar).

Furthermore, sequence analysis demonstrates that ATAT4 is the most divergent sequence with the highest similarity to ATAT10 (18.5%). The highest similarity (15.3%) to a known sequence is with a meadowfoam (*Limnanthes douglassi*) LPAAT. However, the sequences of ATAT4 and ATAT10 share several conserved peptide sequences with the amino acid sequences of ATAT2 and ATAT3 (Figure 2), VXNHXS (SEQ ID NO: 127) where the H comprises the conserved H of the HXXXXD sequence and FXXGAF (SEQ ID NO: 133) downstream of the PEG sequence.

Example 6: Identification of Additional Acyltransferase Sequences

The novel *Arabidopsis* sequences identified above are used to search proprietary databases containing soybean and corn EST sequences. The results of this search identifies EST sequences from soybean (SEQ ID NO:24 through SEQ ID NO: 85) as well as from corn (SEQ ID NO: 86 through SEQ ID NO:126) as encoding acyltransferase related proteins.

Sequence comparisons between the various EST sequences and the complete *Arabidopsis* sequences reveals that the identified EST sequences demonstrate higher similarity to the various *Arabidopsis* sequences as determined by BLAST scores.

Expressed Sequence Tag (EST) sequences from soybean and corn databases are identified which are most closely related by BLAST score to ATAT1 (SEQ ID NOS:24-29 and SEQ ID NOS:86-88, respectively), ATAT2 (SEQ ID NO: 30 and SEQ ID NO:89, respectively), ATAT3 (SEQ ID NOS:31-35 and SEQ ID NOS:90-94, respectively), ATAT4 (SEQ ID NOS:36-44 and SEQ ID NOS:95-100, respectively), ATAT6 (SEQ ID NOS:45-49 and SEQ ID NO:101, respectively), ATAT7 (SEQ ID NOS:50-54 and SEQ ID NOS:102-103, respectively), ATAT8 (SEQ ID NOS:55-56 and SEQ ID NO:104, respectively), ATAT9 (SEQ ID NOS:57-79 and SEQ ID NOS:105-111, respectively), ATAT10 (SEQ ID NOS:80-81 and SEQ ID NO:112, respectively), ATAT11, (SEQ ID NOS:82-85 and SEQ ID NOS:123-126, respectively), and ATLPAAT1 (SEQ ID NOS: 113-122 respectively).

Example 7: Expression Construct Preparation

A series of synthetic oligo nucleotide primers were prepared for use in Polymerase Chain Reactions (PCR) to amplify the entire DNA sequences encoding the various acyltransferase sequences identified above. The sequences are listed in Table 3.

Table 3

Primer	Sequence (listed 5'-3')	SEQ ID NO:
ATAT1F	AAGCTTGCATGCGTCGACACAATGGTTCATGCGACCAAGT CAG	163
ATAT1R	GGTACCGTCGACTCACTTCTTGGTGTTGTTGATAG	164
ATAT2F	GGATCCGCGGCCGCACAATGACGAGCTTTACTACTTCCCT TCAT	165
ATAT2R	GGATCCCCTGCAGGTTAGAGATCCATTGATTCTGCAAT	166
ATAT3F	GGATCCGCGGCCGCATAATGGAATCAGAGCTCAAAGAT	167
ATAT3R	GGATCCCCTGCAGGTCATTCTTCTTTCTGATGGAAATC	168
ATAT4F	GGATCCGCGGCCGCACAATGACTCGTTCACAAGATGTTTC A	169
ATAT4R	GGATCCCCTGCAGGTCACTTCTCTTCCAATCTAGCCAG	170
ATAT6F	GGATCCGCGGCCGCACAATGTCCGGTAATAAGATCTCGAC TCTTCA	171
ATAT6R	GGATCCCCTGCAGGTTATTTTTTCTTGACAACTCCGTTAT TACCGG	172
ATAT7F	ATATCCGCGGCCGCACAATGGTTATGGAGCAAGCTGGAA	173
ATAT7R	GGATCCCCTGCAGGTCAATGGAGACAAGGCTCGAAAGT	174
ATAT8F	GGATCCGCGGCCGCACAATGTCCGCCAAGATTTCAATATT CC	175
ATAT8R	GGATCCCCTGCAGGTTAATTTTTCTTAACTACTCCATT	176
ATAT9F	GGATCCGCGGCCGCACAATGGGAGCTCAGGAGAAACGGCG CC	177
ATAT9R	GGATCCCCTGCAGGTCACGTCTTCTCCTTCTTCACCGG	178
ATAT10F	GGATCCGCGGCCGCACAATGGCGGATCCTGATCTGTCTTC TCCT	179
ATAT10R	GGATCCCCTGCAGGTTATGTTGGGGCCAAGTCAGGTGCAA AGAT	180
ATAT11F	GGATCCGCGGCCGCAAAATGGAAAAAAGAGTGTACCAAA	181

	TTCT	
ATAT11R	GGATCCCCTGCAGGTTATTTGTTTACTAATTTGAGGGAATTTTTTG	182
ATLPAAT 1F	TCGACCTGCAGGAAGCTTAAGGATGGTGATTGCTGC	183
ATLPAAT 1R	GGATCCGCGGCCGCTTACTTCTCCTTCTCCG	184
YSCAT1F	GGATCCGCGGCCGCACAATGTCTTTTAGGGATGTCCTAG	185
YSCAT1R	GGATCCCCTGCAGGTCAATCATCCTTACCCTTTGGTTTACC	186
YSCAT 1 KO F	ATGTCTTTTAGGGATGTCCTAGAAAGAGGAGATGAATTTTCTGTGCGGTATTTCACACCG	187
YSCAT 1 KO R	TCAATCATCCTTACCCTTTGGTTTACCCTCTGGAGGCAGAAGATTGTACTGAGAGTGCAC	188
YSCAT2F	GGATCCGCGGCCGCACAATGAAGCATTCCCAAAAATACCGTAGG	189
YSCAT2R	GGATCCCCTGCAGGTCAATGATTTTTTTTCATCACAAATAC	190
YSCAT 2 KO F	ATGAAGCATTCCCAAAAATACCGTAGGTATGGAATTTATGCTGTGCGGTATTTCACACCG	191
YSCAT 2 KO R	TCAATGATTTTTTTTCATCACAAATACAAGAATAAGAAAAAGATTGTACTGAGAGTGCAC	192
YSCAT 3F	GGATCCGCGGCCGCACAATGGGTTTTGTTGATTTCTTCGAAAC	193
YSCAT 3R	GGATCCCCTGCAGGTTATTTGGTCTCAATTTTAATATTTTTTTGC	194
YSCAT 3 KO F	ATGGGTTTTGTTGATTTCTTCGAAACATATATGGTCGGTTCTGTGCGGTATTTCACACCG	195
YSCAT 3 KO R	TTATTTGGTCTCAATTTTAATATTTTTTTGCAAGGACTCGAGATTGTACTGAGAGTGCAC	196
YSCAT 4F	GGATCCGCGGCCGCACAATGGAAAAGTACACCAATTGGAGAGAC	197
YSCAT 4R	GGATCCCCTGCAGGCTACTTCCTCTTTTTACGTTGATCGCTG	198
YSCAT 4 KO F	ATGGAAAAGTACACCAATTGGAGAGACAATGGTACGGGAACTGTGCGGTATTTCACACCG	199
YSCAT 4 KO R	CTACTTCCTCTTTTTACGTTGATCGCTGATATATTCCTTCAGATTGTACTGAGAGTGCAC	200

YSCAT 5F	GGATCCGCGGCCGCACAATGCCTGCACCAAAACTCACGGA G	201
YSCAT 5R	GGATCCCCTGCAGGCTACGCATCTCCTTCTTTCCCTTC	202
YSCAT 5 KO F	ATGCCTGCACCAAAACTCACGGAGAAATCTGCCTCTTCCA CTGTGCGGTATTTCACACCG	203
YSCAT 5 KO R	CTACGCATCTCCTTCTTTCCCTTCTTCTTCTTCTTCCTCT AGATTGTACTGAGAGTGCAC	204
YSCAT 6F	GGATCCGCGGCCGCACAATGTCTGCTCCCGCTGCCGATCA TAACGC	205
YSCAT 6R	GGATCCCCTGCAGGTCATTCTTTCTTTTCGTGTTCTCTTT TCTG	206
YSCAT 6 KO F	ATGTCTGCTCCCGCTGCCGATCATAACGCTGCCAAACCTA CTGTGCGGTATTTCACACCG	207
YSCAT 6 KO R	TCATTCTTTCTTTTCGTGTTCTCTTTTCTGTCTTACCAGC AGATTGTACTGAGAGTGCAC	208
YSCAT 7F	GGATCCGCGGCCGCACAATGCTGCATCAAAAAATAGCTCA TAAAGTTCG	209
YSCAT 7R	GGATCCCCTGCAGGTCAAAAAATAAAACAATAAAGTTTAT AAACTAACC	210
YSCAT 7 KO F	ATGCTGCATCAAAAAATAGCTCATAAAGTTCGAAAAGTCG CTGTGCGGTATTTCACACCG	211
YSCAT 7 KO R	TCAAAAAATAAAACAATAAAGTTTATAAACTAACCAAATT AGATTGTACTGAGAGTGCAC	212
YSCAT 8F	GGATCCGCGGCCGCACAATGAGTGTGATAGGTAGGTTCTT G	213
YSCAT 8R	GGATCCCCTGCAGGTTAATGCATCTTTTTTACAGATGAAC C	214
YSCAT 8 KO F	ATGAGTGTGATAGGTAGGTTCTTGTATTACTTGAGGTCCG CTGTGCGGTATTTCACACCG	215
YSCAT 8 KO R	TTAATGCATCTTTTTTACAGATGAACCTTCGTTATGGGTA AGATTGTACTGAGAGTGCAC	216

The entire coding regions for each of the acyltransferase sequences were amplified using the respective primers listed in the Table 3 above, cloned into the vector pCR2.1Topo (Invitrogen) or pZero (Invitrogen), and labeled as pCGN8558 (ATAT1), pCGN8564

(ATAT2), pCGB8565 (ATAT3), pCGN8566 (ATAT4), pCGN8918 (ATAT6),

pCGN8913 (ATAT7), pCGN8904 (ATAT8), pCGN9970 (ATAT9), pCGN9940

(ATAT10), pCGN8567 (ATAT11), pCGN8632 (ATLPAAT1), pCGN9901 (YSCAT1

also referred to as gi2132299), pCGN9902 (YSCAT2, also referred to as gi1078509),

pCGN9903 (YSCAT3, also referred to as gi2132939), pCGN9904 (YSCAT4, also

referred to gi21330531), pCGN9905 (YSCAT5, also referred to as gi320748), pCGN9906

(YSCAT6, also referred to as gi549627), pCGN9907 (YSCAT7, also referred to as

gi586485), and pCGN9908 (YSCAT8, also referred to as gi464422). The nucleic acid

sequences for the respective yeast acyltransferase are provided YSCAT1 (SEQ ID

NO:225), YSCAT2 (SEQ ID NO:226), YSCAT3 (SEQ ID NO:227), YSCAT4 (SEQ ID

NO:228), YSCAT5 (SEQ ID NO:229), YSCAT6 (SEQ ID NO:230), YSCAT7 (SEQ ID

NO:231), and YSCAT8 (SEQ ID NO:232).

7A. Baculovirus Expression Constructs

Constructs are prepared to direct the expression of the *Arabidopsis* ATAT sequences in cultured insect cells. The entire coding regions of ATAT1, 2, 3, 4, 6, 7, 8, 9, 10, and 11 are cloned into the vector pFastBac1 (Gibco-BRL, Gaithersburg, MD) digested with *Not*I and

5   *Pst*I. The respective coding sequences were cloned as *Not*I/*Sse*8387I fragments. Double stranded DNA sequence was obtained to verify that no errors were introduced by PCR amplification. The resulting plasmid were designated pCGN9723 (ATAT1), pCGN9724 (ATAT2), pCGN9725 (ATAT3), pCGN9726 (ATAT4), pCGN9727 (ATAT5), pCGN9728 (ATAT7), pCGN9729 (ATAT8), pCGN9991 (ATAT9) pCGN9730 (ATAT10), pCGN9731

10   (ATAT11).

7B. Plant Expression Construct Preparation

A plasmid containing the napin cassette derived from pCGN3223 (described in USPN 5,639,790, the entirety of which is incorporated herein by reference) was modified to make it

15   more useful for cloning large DNA fragments containing multiple restriction sites, and to allow the cloning of multiple napin fusion genes into plant binary transformation vectors. An adapter comprised of the self annealed oligonucleotide of sequence CGCGATTTAAATGGCGCGCCCTGCAGGCGGCCGCCTGCAGGGCGCGCCATTTAA (SEQ ID NO:233) AT was ligated into the cloning vector pBC SK+ (Stratagene) after

20   digestion with the restriction endonuclease BssHII to construct vector pCGN7765. Plamids pCGN3223 and pCGN7765 were digested with NotI and ligated together. The resultant vector, pCGN7770, contains the pCGN7765 backbone with the napin seed specific expression cassette from pCGN3223.

The cloning cassette, pCGN7787, essentially the same regulatory elements as

25   pCGN7770, with the exception of the napin regulatory regions of pCGN7770 have been replaced with the double CAMV 35S promoter and the tml polyadenylation and transcriptional termination region.

A binary vector for plant transformation, pCGN5139, was constructed from pCGN1558 (McBride and Summerfelt, (1990) Plant Molecular Biology, 14:269-276). The

30   polylinker of pCGN1558 was replaced as a HindIII/Asp718 fragment with a polylinker containing unique restriction endonuclease sites, AscI, PacI, XbaI, SwaI, BamHI, and NotI. The Asp718 and HindIII restriction endonuclease sites are retained in pCGN5139.

A series of turbo binary vectors are constructed to allow for the rapid cloning of DNA sequences into binary vectors containing transcriptional initiation regions (promoters) and transcriptional termination regions.

The plasmid pCGN8618 was constructed by ligating oligonucleotides 5'-TCGAGGATCCGCGGCCGCAAGCTTCCTGCAGG-3') (SEQ ID NO:234) and 5'-TCGACCTGCAGGAAGCTTGCGGCCGCGGATCC-3') (SEQ ID NO:235) into SalI/XhoI-digested pCGN7770. A fragment containing the napin promoter, polylinker and napin 3' region was excised from pCGN8618 by digestion with Asp718I; the fragment was blunt-ended by filling in the 5' overhangs with Klenow fragment then ligated into pCGN5139 that had been digested with Asp718I and HindIII and blunt-ended by filling in the 5' overhangs with Klenow fragment. A plasmid containing the insert oriented so that the napin promoter was closest to the blunted Asp718I site of pCGN5139 and the napin 3' was closest to the blunted HindIII site was subjected to sequence analysis to confirm both the insert orientation and the integrity of cloning junctions. The resulting plasmid was designated pCGN8622.

The plasmid pCGN8619 was constructed by ligating oligonucleotides 5'-TCGACCTGCAGGAAGCTTGCGGCCGCGGATCC -3') (SEQ ID NO:236) and 5'-TCGAGGATCCGCGGCCGCAAGCTTCCTGCAGG-3') (SEQ ID NO:237) into SalI/XhoI-digested pCGN7770. A fragment containing the napin promoter, polylinker and napin 3' region was removed from pCGN8619 by digestion with Asp718I; the fragment was blunt-ended by filling in the 5' overhangs with Klenow fragment then ligated into pCGN5139 that had been digested with Asp718I and HindIII and blunt-ended by filling in the 5' overhangs with Klenow fragment. A plasmid containing the insert oriented so that the napin promoter was closest to the blunted Asp718I site of pCGN5139 and the napin 3' was closest to the blunted HindIII site was subjected to sequence analysis to confirm both the insert orientation and the integrity of cloning junctions. The resulting plasmid was designated pCGN8623.

The plasmid pCGN8620 was constructed by ligating oligonucleotides 5'-TCGAGGATCCGCGGCCGCAAGCTTCCTGCAGGAGCT -3') (SEQ ID NO:238) and 5'-CCTGCAGGAAGCTTGCGGCCGCGGATCC-3') (SEQ ID NO:239) into SalI/SacI-digested pCGN7787. A fragment containing the d35S promoter, polylinker and tml 3' region was removed from pCGN8620 by complete digestion with Asp718I and partial digestion with NotI. The fragment was blunt-ended by filling in the 5' overhangs with Klenow fragment then ligated into pCGN5139 that had been digested with Asp718I and HindIII and blunt-ended by filling in the 5' overhangs with Klenow fragment. A plasmid containing the insert

oriented so that the d35S promoter was closest to the blunted Asp718I site of pCGN5139 and the tml 3' was closest to the blunted HindIII site was subjected to sequence analysis to confirm both the insert orientation and the integrity of cloning junctions. The resulting plasmid was designated pCGN8624.

The plasmid pCGN8621 was constructed by ligating oligonucleotides 5'-TCGACCTGCAGGAAGCTTGCGGCCGCGGATCCAGCT -3') (SEQ ID NO:240) and 5'-GGATCCGCGGCCGCAAGCTTCCTGCAGG-3') (SEQ ID NO:241) into SalI/SacI-digested pCGN7787. A fragment containing the d35S promoter, polylinker and tml 3' region was removed from pCGN8621 by complete digestion with Asp718I and partial digestion with NotI. The fragment was blunt-ended by filling in the 5' overhangs with Klenow fragment then ligated into pCGN5139 that had been digested with Asp718I and HindIII and blunt-ended by filling in the 5' overhangs with Klenow fragment. A plasmid containing the insert oriented so that the d35S promoter was closest to the blunted Asp718I site of pCGN5139 and the tml 3' was closest to the blunted HindIII site was subjected to sequence analysis to confirm both the insert orientation and the integrity of cloning junctions. The resulting plasmid was designated pCGN8625.

The coding regions of the various acyltransferase sequences were cloned as NotI/Sse8387I fragments into pCGN8622, pCGN8623, pCGN8624, and pCGN8625, for expression in sense or antisense orientations from a tissue preferential promoter, napin, or the 35S promoter. Fragments which were cloned into the pCGN8622 vector created the constructs pCGN8901 (ATAT1), pCGN8571 (ATAT2), pCGN8909 (ATAT3), pCGN8596 (ATAT4), pCGN8919 (ATAT6), pCGN8914 (ATAT7), pCGN8905 (ATAT8), pCGN9973 (ATAT9), pCGN9942 (ATAT10), pCGN8575 (ATAT11), and pCGN8633 (ATLPAAT1) for the sense expression of the respective coding sequences from the napin promoter. Fragments which were cloned into the pCGN8623 vector created the constructs pCGN8900 (ATAT1), pCGN8572 (ATAT2), pCGN8910 (ATAT3), pCGN8597 (ATAT4), pCGN8920 (ATAT6), pCGN8915 (ATAT7), pCGN8906 (ATAT8), pCGN9972 (ATAT9), pCGN9943 (ATAT10), pCGN8576 (ATAT11), and pCGN8634 (ATLPAAT1) for the antisense expression of the respective coding sequences from the napin promoter. Fragments which were cloned into the pCGN8624 vector created the constructs pCGN8903 (ATAT1), pCGN8573 (ATAT2), pCGN8911 (ATAT3), pCGN8598 (ATAT4), pCGN8921 (ATAT6), pCGN8916 (ATAT7), pCGN8907 (ATAT8), pCGN9971 (ATAT9), pCGN9944 (ATAT10), pCGN8577 (ATAT11), and pCGN8635 (ATLPAAT1) for the sense expression of the respective coding sequences

from the 35S promoter. Fragments which were cloned into the pCGN8625 vector created the constructs pCGN8902 (ATAT1) and pCGN9974 (ATAT9) for the antisense expression of the respective coding sequences from the 35S promoter.

In addition, the yeast acyltransferase coding sequences were cloned into the vector pCGN8624 creating the constructs pCGN9926 (YSCAT1), pCGN9927 (YSCAT2), pCGN9928 (YSCAT3), pCGN9929 (YSCAT4), pCGN9930 (YSCAT5), pCGN9931 (YSCAT6), pCGN9932 (YSCAT7), and pCGN9933 (YSCAT8). These constructs allow for the sense expression of the respective acyltransferase coding sequences from the 35S promoter in plant cells.

Example 8: Plant Transformation

A variety of methods have been developed to insert a DNA sequence of interest into the genome of a plant host to obtain the transcription or transcription and translation of the sequence to effect phenotypic changes.

Transgenic *Brassica* plants are obtained by *Agrobacterium*-mediated transformation as described by Radke *et al.* (*Theor. Appl. Genet.* (1988) *75*:685-694; *Plant Cell Reports* (1992) *11*:499-505). Transgenic *Arabidopsis thaliana* plants may be obtained by *Agrobacterium*-mediated transformation as described by Valverkens *et al.*, (*Proc. Nat. Acad. Sci.* (1988) *85*:5536-5540), or as described by Bent et al. ((1994), *Science* 265:1856-1860), or Bechtold et al. ((1993), *C.R.Acad.Sci, Life Sciences* 316:1194-1199) or Clough, *et al.* (1998) *Plant J.*, 16:735-43. Other plant species may be similarly transformed using related techniques.

Alternatively, microprojectile bombardment methods, such as described by Klein *et al.* (*Bio/Technology 10*:286-291) may also be used to obtain nuclear transformed plants.

The above results demonstrate that the nucleic acid sequences identified encode proteins which are related to protein sequences encoding acyltransferase proteins. Such acyltransferase sequences find use in preparing expression constructs for plant transformations.

All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All

publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

5   Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claim.

Claims

What is Claimed is:

1. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

wherein said enzyme includes the amino acid sequence of SEQ ID NO: 127 (VxNHxS) wherein the H is the conserved Histidine residue in the conserved peptide sequence HXXXXD of said acyltransferase-like protein, x representing any amino acid.

2. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

wherein said enzyme includes the amino acid sequence of SEQ ID NO: 128 (VTYSxS) within about 30 amino acids downstream from the conserved amino acid sequence HXXXXD of said acyltransferase-like protein, x representing any amino acid.

3. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

wherein said enzyme includes the amino acid sequence of SEQ ID NO: 129 (VxLTRxR) within about 60 amino acids downstream from the conserved amino acid sequence HXXXXD of said acyltransferase-like protein, x representing any amino acid.

4. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

wherein said enzyme includes the amino acid sequence of SEQ ID NO: 132 (LxxGDLV) within about 20 amino acids upstream of the conserved amino acid sequence PEG of said acyltransferase-like protein, x representing any amino acid.

5. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

wherein said enzyme includes the amino acid sequence of SEQ ID NO: 130 (CPEGT) containing the conserved amino acid sequence PEG of said acyltransferase-like protein.

6. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

wherein said enzyme includes the amino acid sequence of SEQ ID NO: 133 (FxxGAF) within about 20 amino acids downstream from the conserved amino acid sequence

5   PEG of said acyltransferase-like protein, x representing any amino acid.

7. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

wherein said enzyme includes the amino acid sequence of SEQ ID NO: 131 (IVPVA)

10   within about 40 amino acids downstream from the conserved amino acid sequence PEG of said acyltransferase-like protein.

8. An isolated DNA sequence encoding an enzyme of the class of acyltransferase-like proteins,

15   wherein said enzyme includes the amino acid sequence of SEQ ID NO: 134 (VANxxQ) within about 110 amino acids downstream from the conserved amino acid sequence PEG of said acyltransferase-like protein, x representing any amino acid.

20   9. A DNA sequence encoding an enzyme of the class of acyltransferase-like proteins, said DNA sequence obtainable by the steps comprising:

     (a)   using the profile of Figure 1 to search a nucleic acid sequence database;

     (b)   obtaining a probability score for nucleic acid sequences in said sequence database using the Smith-Waterman algorithm; and

25   (c)   selecting a nucleic acid sequence having a probability score of less than about 1.

10. The DNA encoding sequence according to Claim 9, wherein said DNA sequence is an encoding sequence.

30   11. The DNA encoding sequence according to Claim 9, wherein said DNA sequence is an EST.

12. The DNA encoding sequence according to any one of Claims 1 to 11, wherein said acyltransferase-like protein is from a plant.

13. A construct comprising a DNA sequence of any one of Claims 1 to 11 linked to a
5 heterologous transcriptional and translational initiation region functional in a host cell.

14. The construct according to Claim 13 wherein said host cell is a plant cell.

15. A plant cell comprising a DNA construct according to Claim 13.
10

16. A plant comprising a cell according to Claim 15.

17. The DNA encoding sequence of any one of 1 to 11 wherein said acyltransferase-
15 like protein is from *Arabidopsis thaliana*.

18. The DNA encoding sequence of any one of 1 to 11 wherein said acyltransferase-
like protein is from corn.

20 19. The DNA encoding sequence of Claim 18 wherein said sequence comprises and
EST selected from the group consisting of SEQ ID NO: 86 through SEQ ID NO: 126.

20. The DNA encoding sequence of any one of 1 to 11 wherein said acyltransferase-
like protein is from soybean.
25

21. The DNA encoding sequence of Claim 20 wherein said sequence comprises and
EST selected from the group consisting of SEQ ID NO: 24 through SEQ ID NO: 85.

22. The DNA encoding sequence of any one of Claims 2, 3, 4, 5, 7 and 8 wherein
30 said acyltransferase-like protein is selected from the group consisting of SEQ ID NO: 1, SEQ
ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14 and SEQ ID NO: 16.

23. The DNA encoding sequence of either of Claim 1 and Claim 6 wherein said acyltransferase-like protein is selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7 and SEQ ID NO: 18.

Figure 1/5

Figure 2/5

Figure 3/5

F
W
R
H
C
C
:90
C
P
P
Y
M
A
K
G
E
H
:100
F
W
H
P
F
F
G
W
M
M
:110
W
L
H
G
C
F
F
H
D
R
:120
N
W
K
D
R
K
A

Figure 4/5

Figure 5/5

!1170 A M E A M K R M R K !1180 P D C P H H P V T H !1190 G Y F H L H W P D T !1200 P P H E L

Figure 2
1/3

		10	20	30	40
ATAT1	Y - - T Y E M L G I H L T I R G H R - P P P P S P G T L G N L Y V L N H R T A L D P
ATAT9	N Y K L T G I K L V V N G H P - P P P P K P G Q P G H L V C N H R T V L D P
ATAT7	V - - S - Q I F G G H I I V K G K P - P Q P P A A G K S G V K G C L F V C T H R T L M D P
ATAT8	F S G C R L T V T N D Y V V S S Q K - Q - - K P S A D R K R G C L F V C N H R T L L D P
ATAT6	A F S G I H L T L T - - - V N H N A - D L I S A D R K R G C L F V C N H R S H M D Y
PLSB_ECOLI	N R L Y Q G I N V F F W N I Q V F A D N E T F - - N R M G K E H A L V I S N H R S D I D W
PLSB_MOUSE	S - F F W N I Q V F A D N E T F - - N R M G K E H A L V I S N H R S D I D W
ATLPAAT1	- D W W A G V K I K L F T D P D T F - - R L M G K E H A L I S N H R S D I D W
Jojoba AT	V - D W W A G V K V Q L H A D E E T Y - - R S M G K E H A L I A N H R T E V D W
Maize AT	V - D W W A G V K V Q L H A D E E T Y - - R S M G K E H A L I A N H R T E V D W
ATAT11	L - - W P F L F E K I N K T K V I F S G D K V P C E D R V L Y I C N H A S L V D I
PLSC_COCO	V T G R M L M W I L G N P I T - - I E G S E F S N T R A I Y I S N H A S P - D A
PLSC_LIM	I I G G L V I W I Y G I P P I - K - - I Q G S E H T K K R A I Y I - A N H Q N N Y D M
PLSC_ECOLI	F - G R L A P L - F G L K V - - E C R K P T D A E S Y G N A I Y I - M I A N H Q S T L D I
PLSC_YEAST	F - Y H V M K L M L G L D V - - K V V G E E N L A K K Y V Y Y V S N H Q S F L D I
ATAT2	W A S I Y P F Y K I N I - E - - G L E N L P S S D T P A I V Y V S N H V S Y I E P
ATAT3	M D S N P K T T S T E - - N Q - K G E A A T E E P E R P G A I V Y V S N H L D I
ATAT10	R C I L F S F G - Y Q W - R R - K G K P A R - - R E I A P T V Y V S N H V S Y I E P
ATAT4	M I C S F F V A S - - W - T G V V K Y H G P R P S - I R Q V V A N H T S M I D F

	50	60	70	80
ATAT1	I V A I A L G R K - I C C V T Y S V S R L S L M L S P I P A V A
ATAT9	V V T A V A L G R K - I S C V T Y S I S K F S E L I S P I K A V A
ATAT7	V V L S Y V L G R S - I P A V T Y S I S R L S E L L A P I P T V R
ATAT8	L Y I S A F A L R K K N I K T V T Y S L S R V S K F L L A P I K T V R
ATAT6	L Y I - S Y A L R K N M K A V I T Y P P H I A A G I N L N F W - K T V R
PLSB_ECOLI	L L L S Y V L Y H Q G L V P P H I A A S G N N L N - I P V - G A F F
PLSB_MOUSE	L L L T F I - L F C H N I K A P Y I A A V M K K S S K F L P V - F S T L I H K L G G F F
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Maize AT	L I G W I L A L R K G Q I G N - K Y T - V G K Y W Y P L L G W S M W F A E Y L F
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PLSC_YEAST	F M L G R J F P P G - G K S - F K F I S K T G I F V P I - G W A M S M M G G V V P
ATAT2	Y T L L S L - G K S F P S - - - F V A K R S V G K L P L V - G L I S K C L G C V Y
ATAT3	L Y H M S A S F P S - - - I V A I S E S H D S L P F - G T I I R A M Q V - I Y
ATAT10	I F Y F Y E L S P T - - - V A S E S H D S L P F - G T I I R A M Q V - I E P
ATAT4	I V L E Q M T A F A - - - V I M Q K H P G W V G L Q S T I L E S V G C I I - W

SUBSTITUTE SHEET (RULE 26)

Figure 2
2/3
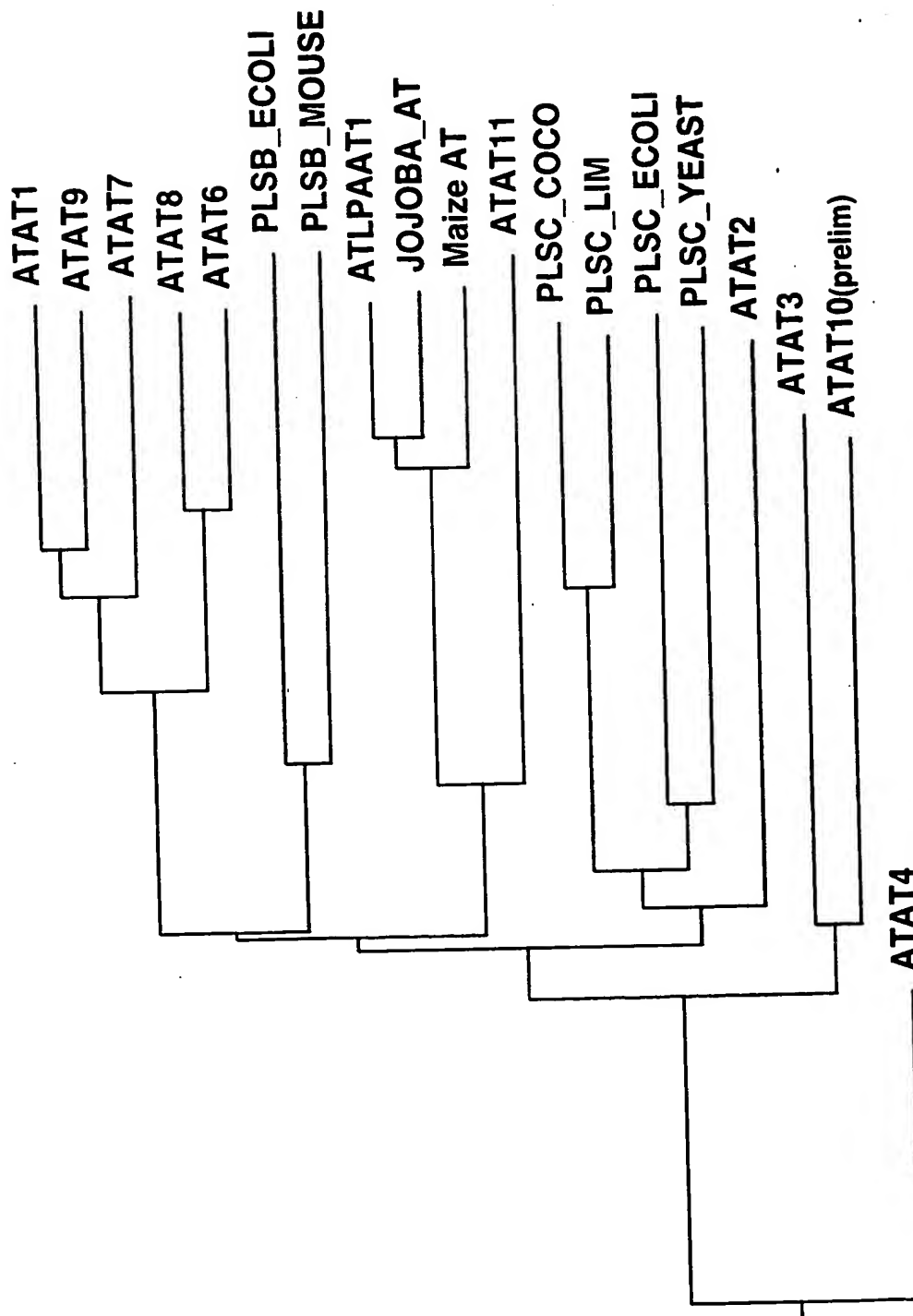
Figure 2
3/3

Figure 3 1/2

Percent Similarity

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1	ATAT1		67.0	58.2	47.2		11.6	11.5	12.0	10.5	12.4	13.4	12.9	12.8	12.3	12.3	11.8	16.3	14.4	14.4	1
2	ATAT9	31.4		63.9	35.8	50.0	12.9	12.4	14.9	14.4	13.9	16.5	11.3	12.4	12.4	11.3	11.2	13.4	13.7	14.4	2
3	ATAT7	40.2	63.9		50.3	48.6	12.9	14.4	14.9	13.4	11.3	12.9	12.4	12.9	11.9	13.9	13.4	13.4	17.1	14.4	3
4	ATAT8	49.7	35.8	50.3		67.2	10.8	13.3	11.8	11.8	10.8	16.4	11.8	11.8	12.8	13.3	12.3	17.4	15.1	12.8	4
5	ATAT6	50.3	50.0	48.6	25.7		12.3	12.3	13.8	12.8	12.3	12.3	12.3	12.8	12.8	12.3	12.8	15.9	13.7	15.9	5
6	PLSB_ECOLI	85.6	50.3	85.6	86.2	86.1		28.5	12.6	12.1	11.6	9.7	13.9	14.3	14.8	11.8	17.6	13.5	12.3	10.6	6
7	PLSB_MOUSE	83.8	86.3	82.8	82.7	84.3	28.5		12.6	12.3	12.9	13.1	12.4	13.3	14.3	13.8	15.0	11.7	11.6	10.0	7
8	ATLPAAT1	82.9	86.8	81.2	83.1	81.2				12.6	78.0	31.6	12.4	12.8	13.3	15.8	13.9	12.2	16.4	14.4	8
9	JOJOBA_AT	83.5	78.4	81.8	85.9	84.6	66.2	85.1	65.4		22.5	32.1	13.9	14.3	13.3	16.3	15.5	12.4	15.1	12.0	9
10	Maize AT	83.5	77.8	84.1	87.6	85.1	83.6	87.1	80.9	65.0		30.6	13.9	16.7	12.8	16.3	14.4	12.9	16.4	12.0	10
11	ATAT11	84.1	82.4	83.1	85.1	85.1	85.6	87.1	79.5	22.5	77.5		14.4	14.8	11.8	12.8	13.4	14.6	15.8	12.9	11
12	PLSC_COCO	83.6	81.4	84.6	83.3	83.2	84.4	87.4	82.1	82.3	67.5	82.4		66.7	27.9	28.4	23.5	14.9	17.1	12.9	12
13	PLSC_LIM	82.1	84.6	81.7	81.0	82.0	90.3	86.8	81.4	80.5	81.1	81.6	33.3		26.1	28.1	19.3	14.8	14.4	15.3	13
14	PLSC_ECOLI	83.2	84.0	85.0	83.6	82.9	84.6	86.9	82.9	81.6	79.5	84.3	71.3	71.6		30.0	19.3	18.7	17.8	12.3	14
15	PLSC_YEAST	83.1	81.4	83.0	79.3	81.0	87.6	86.8	86.4	82.0	80.5	84.1	70.3	70.1	62.8		20.3	15.3	15.1	13.8	15
16	ATAT2	82.7	80.6	83.9	78.4	78.8	89.1	86.1	79.1	82.2	79.8	84.5	72.3	75.0	76.5	73.5		18.2	15.8	17.6	16
17	ATAT3	83.7	82.6	86.6	78.4	80.2	88.2	89.8	87.4	85.5	81.6	84.4	80.1	78.2	78.6	80.6	77.8		30.8	17.2	17
18	ATAT10(prelim)	78.5	82.0	82.5	81.7	81.8	80.8	87.1	79.1	80.5	78.9	82.8	81.8	78.1	76.1	78.1	79.3	64.8		18.5	18
19	ATAT4	84.7	84.8	84.8	84.7	85.5	86.5	83.6	87.4	86.5	87.6	91.0	85.0	83.1	85.7	81.8	83.7	79.4	74.1		19
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Percent Divergence

Figure 3 2/2

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      Emig, Robin A
      Ruezinsky, Diane
      Van Eenennaam, Alison

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Pro Leu Asn Ala Ile Ile Thr Tyr Leu Trp Leu Pro Phe Gly Phe Ile
             35   40   45

Leu Ser Ile Ile Arg Val Tyr Phe Asn Leu Pro Leu Pro Glu Arg Phe
             50   55   60

Val Arg Tyr Thr Tyr Glu Met Leu Gly Ile His Leu Thr Ile Arg Gly
65   70   75   80

His Arg Pro Pro Pro Ser Pro Gly Thr Leu Gly Asn Leu Tyr Val
                    85   90   95

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Pro Leu Asn Ala Ile Ile Thr Tyr Leu Trp Leu Pro Phe Gly Phe Ile
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Leu Ser Ile Ile Arg Val Tyr Phe Asn Leu Pro Leu Pro Glu Arg Phe
     50                  55                  60

Val Arg Tyr Thr Tyr Glu Met Leu Gly Ile His Leu Thr Ile Arg Gly
 65                  70                  75                  80

His Arg Pro Pro Pro Pro Ser Pro Gly Thr Leu Gly Asn Leu Tyr Val
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Leu Asn His Arg Thr Ala Leu Asp Pro Ile Ile Val Ala Ile Ala Leu
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145             150             155                 160

Cys Pro Glu Gly Thr Thr Cys Arg Glu Glu Tyr Leu Leu Arg Phe Ser
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Ala Leu Phe Ala Glu Leu Ser Asp Arg Ile Val Pro Val Ala Met Asn
            180             185             190

Cys Lys Gln Gly Met Phe Asn Gly Thr Thr Val Arg Gly Val Lys Phe
        195             200             205

Trp Asp Pro Tyr Phe Phe Phe Met Asn Pro Arg Pro Ser Tyr Glu Ala
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Thr Phe Leu Asp Arg Leu Pro Glu Glu Met Thr Val Asn Gly Gly Gly
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Lys Thr Pro Ile Glu Val Ala Asn Tyr Val Gln Lys Val Ile Gly Ala
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Val Leu Gly Phe Glu Cys Thr Glu Leu Thr Arg Lys Asp Lys Tyr Leu
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Thr Pro Asp Ser Ser Phe Pro Glu Pro Glu Ile Lys Leu Ser Ser Arg
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Leu Arg Gly Ile Phe Phe Cys Val Val Ala Gly Ile Ser Ala Thr Phe
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Leu Ile Val Leu Met Ile Ile Gly His Pro Phe Val Leu Leu Phe Asp
            100   105   110

Pro Tyr Arg Arg Lys Phe His His Phe Ile Ala Lys Leu Trp Ala Ser
        115   120   125

Ile Ser Ile Tyr Pro Phe Tyr Lys Ile Asn Ile Glu Gly Leu Glu Asn
        130   135   140

Leu Pro Ser Ser Asp Thr Pro Ala Val Tyr Val Ser Asn His Gln Ser
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Phe Leu Asp Ile Tyr Thr Leu Leu Ser Leu Gly Lys Ser Phe Lys Phe
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Ile Ser Lys Thr Gly Ile Phe Val Ile Pro Ile Ile Gly Trp Ala Met
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        195   200   205

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225   230   235   240

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Lys Leu Ala Val Ala Leu Val Thr Leu Val Pro Leu Arg Phe Leu Leu
65                  70                  75                  80

Ser Met Ser Ile Leu Leu Leu Tyr Tyr Leu Ile Cys Arg Val Phe Thr
                85                  90                  95

Leu Phe Ser Ala Pro Tyr Arg Gly Pro Glu Glu Glu Glu Asp Glu Gly
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1131
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<212> PRT
<213> Arabidopsis sp.

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            20                 25                  30
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Asn Glu Pro Arg Gly Lys Leu Ser Leu Arg Asp Leu Leu Asp Ile Ser
        35              40              45
Pro Thr Leu Thr Glu Ala Ala Gly Ala Ile Val Asp Asp Ser Phe Thr
        50              55              .60
Arg Cys Phe Lys Ser Asn Pro Pro Glu Pro Trp Asn Trp Asn Ile Tyr
65              70              75              80
Leu Phe Pro Leu Tyr Cys Phe Gly Val Val Val Arg Tyr Cys Ile Leu
            85              90              95
Phe Pro Leu Arg Cys Phe Thr Leu Ala Phe Gly Trp Ile Ile Phe Leu
        100             105             110
Ser Leu Phe Ile Pro Val Asn Ala Leu Leu Lys Gly Gln Asp Arg Leu
        115             120             125
Arg Lys Lys Ile Glu Arg Val Leu Val Glu Met Ile Cys Ser Phe Phe
    130             135             140
Val Ala Ser Trp Thr Gly Val Val Lys Tyr His Gly Pro Arg Pro Ser
145             150             155             160
Ile Arg Pro Lys Gln Val Tyr Val Ala Asn His Thr Ser Met Ile Asp
            165             170             175
Phe Ile Val Leu Glu Gln Met Thr Ala Phe Ala Val Ile Met Gln Lys
        180             185             190
His Pro Gly Trp Val Gly Leu Leu Gln Ser Thr Ile Leu Glu Ser Val
    195             200             205
Gly Cys Ile Trp Phe Asn Arg Ser Glu Ala Lys Asp Arg Glu Ile Val
210             215             220
Ala Lys Lys Leu Arg Asp His Val Gln Gly Ala Asp Ser Asn Pro Leu
225             230             235             240
Leu Ile Phe Pro Glu Gly Thr Cys Val Asn Asn Asn Tyr Thr Val Met
            245             250             255
Phe Lys Lys Gly Ala Phe Glu Leu Asp Cys Thr Val Cys Pro Ile Ala
        260             265             270
Ile Lys Tyr Asn Lys Ile Phe Val Asp Ala Phe Trp Asn Ser Arg Lys
        275             280             285
Gln Ser Phe Thr Met His Leu Leu Gln Leu Met Thr Ser Trp Ala Val
    290             295             300
Val Cys Glu Val Trp Tyr Leu Glu Pro Gln Thr Ile Arg Pro Gly Glu
305             310             315             320
Thr Gly Ile Glu Phe Ala Glu Arg Val Arg Asp Met Ile Ser Leu Arg
            325             330             335
Ala Gly Leu Lys Lys Val Pro Trp Asp Gly Tyr Leu Lys Tyr Ser Arg
        340             345             350
Pro Ser Pro Lys His Ser Glu Arg Lys Gln Gln Ser Phe Ala Glu Ser
        355             360             365
Ile Leu Ala Arg Leu Glu Glu Lys
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<211> 965

<212> DNA
<213> Arabidopsis sp.

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<212> DNA
<213> Arabidopsis sp.

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<210> 11
<211> 530
<212> PRT

<213> Arabidopsis sp.

<400> 11

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          20   25   30

Lys Tyr Gln Lys Cys Pro Ser His Gly Leu His Gln Tyr Gln Asp Leu
        35   40   45

Ser Asn His Thr Leu Ile Phe Asn Val Glu Gly Ala Leu Leu Lys Ser
    50   55   60

Asn Ser Leu Phe Pro Tyr Phe Met Val Val Ala Phe Glu Ala Gly Gly
65   70   75   80

Val Ile Arg Ser Leu Phe Leu Leu Val Leu Tyr Pro Phe Ile Ser Leu
            85   90   95

Met Ser Tyr Glu Met Gly Leu Lys Thr Met Val Met Leu Ser Phe Phe
        100   105   110

Gly Val Lys Lys Glu Ser Phe Arg Val Gly Lys Ser Val Leu Pro Lys
        115   120   125

Tyr Phe Leu Glu Asp Val Gly Leu Glu Met Phe Gln Val Leu Lys Arg
    130   135   140

Gly Gly Lys Arg Val Ala Val Ser Asp Leu Pro Gln Val Met Ile Asp
145   150   155   160

Val Phe Leu Arg Asp Tyr Leu Glu Ile Glu Val Val Val Gly Arg Asp
                165   170   175

Met Lys Met Val Gly Gly Tyr Tyr Leu Gly Ile Val Glu Asp Lys Lys
            180   185   190

Asn Leu Glu Ile Ala Phe Asp Lys Val Val Gln Glu Glu Arg Leu Gly
        195   200   205

Ser Gly Arg Arg Leu Ile Gly Ile Thr Ser Phe Asn Ser Pro Ser His
    210   215   220

Arg Ser Leu Phe Ser Gln Phe Cys Gln Glu Ile Tyr Phe Val Arg Asn
225   230   235   240

Ser Asp Lys Lys Ser Trp Gln Thr Leu Pro Gln Asp Gln Tyr Pro Lys
            245   250   255

Pro Leu Ile Phe His Asp Gly Arg Leu Ala Val Lys Pro Thr Pro Leu
            260   265   270

Asn Thr Leu Val Leu Phe Met Trp Ala Pro Phe Ala Ala Val Leu Ala
        275   280   285

Ala Ala Arg Leu Val Phe Gly Leu Asn Leu Pro Tyr Ser Leu Ala Asn
    290   295   300

Pro Phe Leu Ala Phe Ser Gly Ile His Leu Thr Leu Thr Val Asn Asn
305   310   315   320

His Asn Asp Leu Ile Ser Ala Asp Arg Lys Arg Gly Cys Leu Phe Val
            325   330   335

Cys Asn His Arg Thr Leu Leu Asp Pro Leu Tyr Ile Ser Tyr Ala Leu
            340   345   350

Arg Lys Lys Asn Met Lys Ala Val Thr Tyr Ser Leu Ser Arg Leu Ser

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              355                  360                  365
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Glu Leu Leu Ala Pro Ile Lys Thr Val Arg Leu Thr Arg Asp Arg Val
    370   375   380

Lys Asp Gly Gln Ala Met Glu Lys Leu Leu Ser Gln Gly Asp Leu Val
385   390   395   400

Val Cys Pro Glu Gly Thr Thr Cys Arg Glu Pro Tyr Leu Leu Arg Phe
            405   410   415

Ser Pro Leu Phe Ser Glu Val Cys Asp Val Ile Val Pro Val Ala Ile
        420   425   430

Asp Ser His Val Thr Phe Phe Tyr Gly Thr Thr Ala Ser Gly Leu Lys
        435   440   445

Ala Phe Asp Pro Ile Phe Phe Leu Leu Asn Pro Phe Pro Ser Tyr Thr
    450   455   460

Val Lys Leu Leu Asp Pro Val Ser Gly Ser Ser Ser Ser Thr Cys Arg
465   470   475   480

Gly Val Pro Asp Asn Gly Lys Val Asn Phe Glu Val Ala Asn His Val
            485   490   495

Gln His Glu Ile Gly Asn Ala Leu Gly Phe Glu Cys Thr Asn Leu Thr
            500   505   510

Arg Arg Asp Lys Tyr Leu Ile Leu Ala Gly Asn Asn Gly Val Val Lys
            515   520   525

Lys Lys
530

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<211> 1509
<212> DNA
<213> Arabidopsis sp.

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1320
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<211> 502
<212> PRT
<213> Arabidopsis sp.

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Phe Glu Gly Thr Ile Leu Lys Asn Ala Asp Ser Phe Ser Tyr Phe Met
                20   25   30

Leu Val Ala Phe Glu Ala Ala Gly Leu Ile Arg Phe Ala Ile Leu Leu
            35   40   45

Phe Leu Trp Pro Val Ile Thr Leu Leu Asp Val Phe Ser Tyr Lys Asn
        50   55   60

Ala Ala Leu Lys Leu Lys Ile Phe Val Ala Thr Val Gly Leu Arg Glu
65   70   75   80

Pro Glu Ile Glu Ser Val Ala Arg Ala Val Leu Pro Lys Phe Tyr Met
                85   90   95

Asp Asp Val Ser Met Asp Thr Trp Arg Val Phe Ser Ser Cys Lys Lys
                100   105   110

Arg Val Val Val Thr Arg Met Pro Arg Val Met Val Glu Arg Phe Ala
            115   120   125

Lys Glu His Leu Arg Ala Asp Glu Val Ile Gly Thr Glu Leu Ile Val
        130   135   140

Asn Arg Phe Gly Phe Val Thr Gly Leu Ile Arg Glu Thr Asp Val Asp
145   150   155   160

Gln Ser Ala Leu Asn Arg Val Ala Asn Leu Phe Val Gly Arg Arg Pro
                165   170   175

Gln Leu Gly Leu Gly Lys Pro Ala Leu Thr Ala Ser Thr Asn Phe Leu
            180   185   190

Ser Leu Cys Glu Glu His Ile His Ala Pro Ile Pro Glu Asn Tyr Asn
            195   200   205

His Gly Asp Gln Gln Leu Gln Leu Arg Pro Leu Pro Val Ile Phe His
        210   215   220

Asp Gly Arg Leu Val Lys Arg Pro Thr Pro Ala Thr Ala Leu Ile Ile
225   230   235   240

Leu Leu Trp Ile Pro Phe Gly Ile Ile Leu Ala Val Ile Arg Ile Phe
                245   250   255

Leu Gly Ala Val Leu Pro Leu Trp Ala Thr Pro Tyr Val Ser Gln Ile
                260   265   270

Phe Gly Gly His Ile Ile Val Lys Gly Lys Pro Pro Gln Pro Pro Ala
            275   280   285

Ala Gly Lys Ser Gly Val Leu Phe Val Cys Thr His Arg Thr Leu Met

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           290                    295                    300
Asp Pro Val Val Leu Ser Tyr Val Leu Gly Arg Ser Ile Pro Ala Val
305                  310                  315                  320

Thr Tyr Ser Ile Ser Arg Leu Ser Glu Ile Leu Ser Pro Ile Pro Thr
                 325                  330                  335

Val Arg Leu Thr Arg Ile Arg Asp Val Asp Ala Ala Lys Ile Lys Gln
             340                  345                  350

Gln Leu Ser Lys Gly Asp Leu Val Val Cys Pro Glu Gly Thr Thr Cys
             355                  360                  365

Arg Glu Pro Phe Leu Leu Arg Phe Ser Ala Leu Phe Ala Glu Leu Thr
    370                  375                  380

Asp Arg Ile Val Pro Val Ala Met Asn Tyr Arg Val Gly Phe Phe His
385                  390                  395                  400

Ala Thr Thr Ala Arg Gly Trp Lys Gly Leu Asp Pro Ile Phe Phe Phe
                 405                  410                  415

Met Asn Pro Arg Pro Val Tyr Glu Ile Thr Phe Leu Asn Gln Leu Pro
             420                  425                  430

Met Glu Ala Thr Cys Ser Ser Gly Lys Ser Pro His Asp Val Ala Asn
        435                  440                  445

Tyr Val Gln Arg Ile Leu Ala Ala Thr Leu Gly Phe Glu Cys Thr Asn
    450                  455                  460

Phe Thr Arg Lys Asp Lys Tyr Arg Val Leu Ala Gly Asn Asp Gly Thr
465                  470                  475                  480

Val Ser Tyr Leu Ser Leu Leu Asp Gln Leu Lys Lys Val Val Ser Thr
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Phe Glu Pro Cys Leu His
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<211> 1563
<212> DNA
<213> Arabidopsis sp.

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1140
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<210> 15
<211> 520
<212> PRT
<213> Arabidopsis sp.

<400> 15

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Arg Phe Ile Leu Arg Arg Tyr Arg Asn Ser Lys Pro Lys Tyr Gln Asn
                20                  25                  30

Gly Pro Ser Ser Leu Leu Gln Ser Asp Leu Ser Arg His Thr Leu Ile
            35                  40                  45

Phe Asn Val Glu Gly Ala Leu Leu Lys Ser Asp Ser Leu Phe Pro Tyr
        50                  55                  60

Phe Met Leu Val Ala Phe Glu Ala Gly Gly Val Ile Arg Ser Phe Leu
 65                  70                  75                  80

Leu Phe Ile Leu Tyr Pro Leu Ile Ser Leu Met Ser His Glu Met Gly
                85                  90                  95

Val Lys Val Met Val Met Val Ser Phe Phe Gly Ile Lys Lys Glu Gly
                100                 105                 110

Phe Arg Ala Gly Arg Ala Val Leu Pro Lys Tyr Phe Leu Glu Asp Val
            115                 120                 125

Gly Leu Glu Ile Phe Glu Val Leu Lys Arg Gly Gly Lys Lys Ile Gly
        130                 135                 140

Val Ser Asp Asp Leu Pro Gln Val Met Ile Glu Gly Phe Leu Arg Asp
145                 150                 155                 160

Tyr Leu Glu Ile Asp Val Val Val Gly Arg Glu Met Lys Val Val Gly
                165                 170                 175

Gly Tyr Tyr Leu Gly Ile Met Glu Asp Lys Thr Lys His Asp Leu Val
            180                 185                 190

Phe Asp Glu Leu Val Arg Lys Glu Arg Leu Asn Thr Gly Arg Val Ile
            195                 200                 205

Gly Ile Thr Ser Phe Asn Thr Ser Leu His Arg Tyr Leu Phe Ser Gln
        210                 215                 220

Phe Cys Gln Glu Ile Tyr Phe Val Lys Lys Ser Asp Lys Arg Ser Trp
225                 230                 235                 240

Gln Thr Leu Pro Arg Ser Gln Tyr Pro Lys Pro Leu Ile Phe His Asp
                245                 250                 255
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Gly Arg Leu Ala Ile Lys Pro Thr Leu Met Asn Thr Leu Val Leu Phe
        260   265   270

Met Trp Gly Pro Phe Ala Ala Ala Ala Ala Ala Arg Leu Phe Val
        275   280   285

Ser Leu Cys Ile Pro Tyr Ser Leu Ser Ile Pro Ile Leu Ala Phe Ser
        290   295   300

Gly Cys Arg Leu Thr Val Thr Asn Asp Tyr Val Ser Ser Gln Lys Gln
305   310   315   320

Lys Pro Ser Gln Arg Lys Gly Cys Leu Phe Val Cys Asn His Arg Thr
                325   330   335

Leu Leu Asp Pro Leu Tyr Val Ala Phe Ala Leu Arg Lys Lys Asn Ile
        340   345   350

Lys Thr Val Thr Tyr Ser Leu Ser Arg Val Ser Glu Ile Leu Ala Pro
        355   360   365

Ile Lys Thr Val Arg Leu Thr Arg Asp Arg Val Ser Asp Gly Gln Ala
        370   375   380

Met Glu Lys Leu Leu Thr Glu Gly Asp Leu Val Val Cys Pro Glu Gly
385   390   395   400

Thr Thr Cys Arg Glu Pro Tyr Leu Leu Arg Phe Ser Pro Leu Phe Thr
                405   410   415

Glu Val Ser Asp Val Ile Val Pro Val Ala Val Thr Val His Val Thr
                420   425   430

Phe Phe Tyr Gly Thr Thr Ala Ser Gly Leu Lys Ala Leu Asp Pro Leu
        435   440   445

Phe Phe Leu Leu Asp Pro Tyr Pro Thr Tyr Thr Ile Gln Phe Leu Asp
        450   455   460

Pro Val Ser Gly Ala Thr Cys Gln Asp Pro Asp Gly Lys Leu Lys Phe
465   470   475   480

Glu Val Ala Asn Asn Val Gln Ser Asp Ile Gly Lys Ala Leu Asp Phe
                485   490   495

Glu Cys Thr Ser Leu Thr Arg Lys Asp Lys Tyr Leu Ile Leu Ala Gly
                500   505   510

Asn Asn Gly Val Val Lys Lys Asn
        515   520

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<211> 1506
<212> DNA
<213> Arabidopsis sp.

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1380
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<210> 17
<211> 500
<212> PRT
<213> Arabidopsis sp.

<400> 17
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 1               5                  10                  15

Asp Val Lys Asp Arg Ser Asn His Thr Val Ala Ala Asp Leu Asp Gly
                20                  25                  30

Thr Leu Leu Ile Ser Arg Ser Ala Phe Pro Tyr Tyr Phe Leu Val Ala
        35                  40                  45

Leu Glu Ala Gly Ser Leu Leu Arg Ala Leu Ile Leu Leu Val Ser Val
    50                  55                  60

Pro Phe Val Tyr Leu Thr Tyr Leu Thr Ile Ser Glu Thr Leu Ala Ile
65                  70                  75                  80

Asn Val Phe Val Phe Ile Thr Phe Ala Gly Leu Lys Ile Arg Asp Val
                85                  90                  95

Glu Leu Val Val Arg Ser Val Leu Pro Arg Phe Tyr Ala Glu Asp Val
                100                 105                 110

Arg Pro Asp Thr Trp Arg Ile Phe Asn Thr Phe Gly Lys Arg Tyr Ile
            115                 120                 125

Ile Thr Ala Ser Pro Arg Ile Met Val Glu Pro Phe Val Lys Thr Phe
    130                 135                 140

Leu Gly Val Asp Lys Val Leu Gly Thr Glu Leu Glu Val Ser Lys Ser
145                 150                 155                 160

Gly Arg Ala Thr Gly Phe Thr Arg Lys Pro Gly Ile Leu Val Gly Gln
                165                 170                 175

Tyr Lys Arg Asp Val Val Leu Arg Glu Phe Gly Gly Leu Ala Ser Asp
            180                 185                 190

Leu Pro Asp Leu Gly Leu Gly Asp Ser Lys Thr Asp His Asp Phe Met
            195                 200                 205
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Ser Ile Cys Lys Glu Gly Tyr Met Val Pro Arg Thr Lys Cys Glu Pro
210             215             220

Leu Pro Arg Asn Lys Leu Leu Ser Pro Ile Ile Phe His Glu Gly Arg
225             230             235             240

Leu Val Gln Arg Pro Thr Pro Leu Val Ala Leu Leu Thr Phe Leu Trp
            245             250             255

Leu Pro Val Gly Phe Val Leu Ser Ile Ile Arg Val Tyr Thr Asn Ile
            260             265             270

Pro Leu Pro Glu Arg Ile Ala Arg Tyr Asn Tyr Lys Leu Thr Gly Ile
            275             280             285

Lys Leu Val Val Asn Gly His Pro Pro Pro Pro Lys Pro Gly Gln
290             295             300

Pro Gly His Leu Leu Val Cys Asn His Arg Thr Val Leu Asp Pro Val
305             310             315             320

Val Thr Ala Val Ala Leu Gly Arg Lys Ile Ser Cys Val Thr Tyr Ser
            325             330             335

Ile Ser Lys Phe Ser Glu Leu Ile Ser Pro Ile Lys Ala Val Ala Leu
            340             345             350

Thr Arg Gln Arg Glu Lys Asp Ala Ala Asn Ile Lys Arg Leu Leu Glu
            355             360             365

Glu Gly Asp Leu Val Ile Cys Pro Glu Gly Thr Thr Cys Arg Glu Pro
370             375             380

Phe Leu Leu Arg Phe Ser Ala Leu Phe Ala Glu Leu Thr Asp Arg Ile
385             390             395             400

Val Pro Val Ala Ile Asn Thr Lys Gln Ser Met Phe Asn Gly Thr Thr
            405             410             415

Thr Arg Gly Tyr Lys Leu Leu Asp Pro Tyr Phe Ala Phe Met Asn Pro
            420             425             430

Arg Pro Thr Tyr Glu Ile Thr Phe Leu Lys Gln Ile Pro Ala Glu Leu
            435             440             445

Thr Cys Lys Gly Gly Lys Ser Pro Ile Glu Val Ala Asn Tyr Ile Gln
450             455             460

Arg Val Leu Gly Gly Thr Leu Gly Phe Glu Cys Thr Asn Phe Thr Arg
465             470             475             480

Lys Asp Lys Tyr Ala Met Leu Ala Gly Thr Asp Gly Arg Val Pro Val
            485             490             495

Lys Lys Glu Lys
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<211> 1620
<212> DNA
<213> Arabidopsis sp.

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gttgttgacc ctcgtgtttc acgaggtttt gagtttgacc atcttaatcc ttatggcttt 180
ctcagcgagt cagagcctcc ggttctcggt ccgacgacgg tggatccatt ccggaacaat 240
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tggattactc ggatctgtac cagatgtatc ctcttctctt ttggctatca gtggataaga 480
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gatagatttc ctcgtctgct gttattcccc gaaggaacca cgactaatgg gaaagttctt 780
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1140
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1260
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1380
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<210> 19
<211> 539
<212> PRT
<213> Arabidopsis sp.

<400> 19

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  1               5                  10                  15

Asp Gln Pro Glu Val Val Ile Ser Ile Ala Asp Asp Asp Asp Glu
             20                  25                  30

Ser Gly Leu Asn Leu Leu Pro Ala Val Val Asp Pro Arg Val Ser Arg
        35                  40                  45

Gly Phe Glu Phe Asp His Leu Asn Pro Tyr Gly Phe Leu Ser Glu Ser
    50                  55                  60

Glu Pro Pro Val Leu Gly Pro Thr Thr Val Asp Pro Phe Arg Asn Asn
65                  70                  75                  80

Thr Pro Gly Val Ser Gly Leu Tyr Glu Ala Ile Lys Leu Val Ile Cys
                85                  90                  95

Leu Pro Ile Ala Leu Ile Arg Leu Val Leu Phe Ala Ala Ser Leu Ala
            100                 105                 110

Val Gly Tyr Leu Ala Thr Lys Leu Ala Leu Ala Gly Trp Lys Asp Lys
        115                 120                 125

Glu Asn Pro Met Pro Leu Trp Arg Cys Arg Ile Met Trp Ile Thr Arg
    130                 135                 140

Ile Cys Thr Arg Cys Ile Leu Phe Ser Phe Gly Tyr Gln Trp Ile Arg
145                 150                 155                 160
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Arg Lys Gly Lys Pro Ala Arg Arg Glu Ile Ala Pro Ile Val Val Ser
            165   170   175

Asn His Val Ser Tyr Ile Glu Pro Ile Phe Tyr Phe Tyr Glu Leu Ser
            180   185   190

Pro Thr Ile Val Ala Ser Glu Ser His Asp Ser Leu Pro Phe Val Gly
            195   200   205

Thr Ile Ile Arg Ala Met Gln Val Ile Tyr Val Asn Arg Phe Ser Gln
    210   215   220

Thr Ser Arg Lys Asn Ala Val His Glu Ile Lys Arg Lys Ala Ser Cys
225   230   235   240

Asp Arg Phe Pro Arg Leu Leu Leu Phe Pro Glu Gly Thr Thr Thr Asn
            245   250   255

Gly Lys Val Leu Ile Ser Phe Gln Leu Gly Ala Phe Ile Pro Gly Tyr
            260   265   270

Pro Ile Gln Pro Val Val Val Arg Tyr Pro His Val His Phe Asp Gln
            275   280   285

Ser Trp Gly Asn Ile Ser Leu Leu Thr Leu Met Phe Arg Met Phe Thr
            290   295   300

Gln Phe His Asn Phe Met Glu Val Glu Tyr Leu Pro Val Ile Tyr Pro
305   310   315   320

Ser Glu Lys Gln Lys Gln Asn Ala Val Arg Leu Ser Gln Lys Thr Ser
            325   330   335

His Ala Ile Ala Thr Ser Leu Asn Val Val Gln Thr Ser His Ser Phe
            340   345   350

Ala Asp Leu Met Leu Leu Asn Lys Ala Thr Glu Leu Lys Leu Glu Asn
            355   360   365

Pro Ser Asn Tyr Met Val Glu Met Ala Arg Val Glu Ser Leu Phe His
    370   375   380

Val Ser Ser Leu Glu Ala Thr Arg Phe Leu Asp Thr Phe Val Ser Met
385   390   395   400

Ile Pro Asp Ser Ser Gly Arg Val Arg Leu His Asp Phe Leu Arg Gly
            405   410   415

Leu Lys Leu Lys Pro Cys Pro Leu Ser Lys Arg Ile Phe Glu Phe Ile
            420   425   430

Asp Val Glu Lys Val Gly Ser Ile Thr Phe Lys Gln Phe Leu Phe Ala
            435   440   445

Ser Gly His Val Leu Thr Gln Pro Leu Phe Lys Gln Thr Cys Glu Leu
            450   455   460

Ala Phe Ser His Cys Asp Ala Asp Gly Asp Gly Tyr Ile Thr Ile Gln
465   470   475   480

Glu Leu Gly Glu Ala Leu Lys Asn Thr Ile Pro Asn Leu Asn Lys Asp
            485   490   495

Glu Ile Arg Gly Met Tyr His Leu Leu Asp Asp Asp Gln Asp Gln Arg
            500   505   510

Ile Ser Gln Asn Asp Leu Leu Ser Cys Leu Arg Arg Asn Pro Leu Leu
            515   520   525

Ile Ala Ile Phe Ala Pro Asp Leu Ala Pro Thr

530   535

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<211> 1128
<212> DNA
<213> Arabidopsis sp.

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gttatcttct ctggtgataa ggttccttgc gaggatcgag tattgctcat tgcaaaccac 300
cgaacagaag ttgattggat gtacttctgg gatcttgcac tgcgtaaagg ccagattggg 360
aatatcaaat atgtgcttaa gagtagtttg atgaaattac ctctcttttg ttgggcgttt 420
cacctctttg agtttattcc tgttgagagg agatgggaag tcgatgaagc aaacttgaga 480
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cttccgatac tgaacaacgt gctgcttccc aggacaaaag gtttcgtctc ctgcttgcaa 660
gaactgagtt gctcacttga cgcagtttat gatgtgacca tcggttataa aacccgctgc 720
ccatctttct tagacaacgt ttatggaatt gagccatcag aagttcacat ccacatccgt 780
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1128

<210> 21
<211> 375
<212> PRT
<213> Arabidopsis sp.

<400> 21
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 1   5   10   15

Val Leu Arg Gly Ile Ile Cys Leu Met Val Leu Val Ser Thr Ala Phe
                 20   25   30

Met Met Leu Ile Phe Trp Gly Phe Leu Ser Ala Val Val Leu Arg Leu
             35   40   45

Phe Ser Ile Arg Tyr Ser Arg Lys Cys Val Ser Phe Phe Phe Gly Ser
         50   55   60

Trp Leu Ala Leu Trp Pro Phe Leu Phe Glu Lys Ile Asn Lys Thr Lys
 65   70   75   80

Val Ile Phe Ser Gly Asp Lys Val Pro Cys Glu Asp Arg Val Leu Leu
                 85   90   95

Ile Ala Asn His Arg Thr Glu Val Asp Trp Met Tyr Phe Trp Asp Leu
                100   105   110

Ala Leu Arg Lys Gly Gln Ile Gly Asn Ile Lys Tyr Val Leu Lys Ser
             115   120   125

Ser Leu Met Lys Leu Pro Leu Phe Gly Trp Ala Phe His Leu Phe Glu
         130   135   140

Phe Ile Pro Val Glu Arg Arg Trp Glu Val Asp Glu Ala Asn Leu Arg
145   150   155   160

Gln Ile Val Ser Ser Phe Lys Asp Pro Arg Asp Ala Leu Trp Leu Ala
                165   170   175

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Leu Phe Pro Glu Gly Thr Asp Tyr Thr Glu Ala Lys Cys Gln Arg Ser
        180             185                 190

Lys Lys Phe Ala Ala Glu Asn Gly Leu Pro Ile Leu Asn Asn Val Leu
        195             200                 205

Leu Pro Arg Thr Lys Gly Phe Val Ser Cys Leu Gln Glu Leu Ser Cys
    210             215             220

Ser Leu Asp Ala Val Tyr Asp Val Thr Ile Gly Tyr Lys Thr Arg Cys
225             230             235                 240

Pro Ser Phe Leu Asp Asn Val Tyr Gly Ile Glu Pro Ser Glu Val His
            245             250                 255

Ile His Ile Arg Arg Ile Asn Leu Thr Gln Ile Pro Asn Gln Glu Lys
            260             265                 270

Asp Ile Asn Ala Trp Leu Met Asn Thr Phe Gln Leu Lys Asp Gln Leu
        275             280             285

Leu Asn Asp Phe Tyr Ser Asn Gly His Phe Pro Asn Glu Gly Thr Glu
    290             295             300

Lys Glu Phe Asn Thr Lys Lys Tyr Leu Ile Asn Cys Leu Ala Val Ile
305             310             315                 320

Ala Phe Thr Thr Ile Cys Thr His Leu Thr Phe Phe Ser Ser Met Ile
            325             330             335

Trp Phe Arg Ile Tyr Val Ser Leu Ala Cys Val Tyr Leu Thr Ser Ala
        340             345             350

Thr His Phe Asn Leu Arg Ser Val Pro Leu Val Glu Thr Ala Lys Asn
        355             360             365

Ser Leu Lys Leu Val Asn Lys
370             375
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<210> 22
<211> 1170
<212> DNA
<213> Arabidopsis sp.

<400> 22
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tacagaaaaa ttaaccgggt ggttgcagaa accttgtggt tggagcttgt atggatagtt 180
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cctcgcacca aaggtttcgt gtcagctgtt agtaatatgc gttcatttgt cccagcaatt 660
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tcgaccccag ccaaagtcgt cccagccaag ccaaaagaca atcaccaccc agaatcatcc 1140
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1170

<210> 23
<211> 389
<212> PRT
<213> Arabidopsis sp.

<400> 23

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Met Val Ile Ala Ala Ala Val Ile Val Pro Leu Gly Leu Leu Phe Phe
1               5                   10                  15

Ile Ser Gly Leu Ala Val Asn Leu Phe Gln Ala Val Cys Tyr Val Leu
            20                  25                  30

Ile Arg Pro Leu Ser Lys Asn Thr Tyr Arg Lys Ile Asn Arg Val Val
        35                  40                  45

Ala Glu Thr Leu Trp Leu Glu Leu Val Trp Ile Val Asp Trp Trp Ala
    50                  55                  60

Gly Val Lys Ile Gln Val Phe Ala Asp Asn Glu Thr Phe Asn Arg Met
65              70                  75                  80

Gly Lys Glu His Ala Leu Val Val Cys Asn His Arg Ser Asp Ile Asp
            85                  90                  95

Trp Leu Val Gly Trp Ile Leu Ala Gln Arg Ser Gly Cys Leu Gly Ser
            100                 105                 110

Ala Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile Gly
        115                 120                 125

Trp Ser Met Trp Phe Ser Glu Tyr Leu Phe Leu Glu Arg Asn Trp Ala
        130                 135                 140

Lys Asp Glu Ser Thr Leu Lys Ser Gly Leu Gln Arg Leu Ser Asp Phe
145                 150                 155                 160

Pro Arg Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe Thr
                165                 170                 175

Glu Ala Lys Leu Lys Ala Ala Gln Glu Tyr Ala Ala Ser Ser Glu Leu
            180                 185                 190

Pro Ile Pro Arg Asn Val Leu Ile Pro Arg Thr Lys Gly Phe Val Ser
        195                 200                 205

Ala Val Ser Asn Met Arg Ser Phe Val Pro Ala Ile Tyr Asp Met Thr
    210                 215                 220

Val Thr Ile Pro Lys Thr Ser Pro Pro Pro Thr Met Leu Arg Leu Phe
225                 230                 235                 240

Lys Gly Gln Pro Ser Val Val His Val His Ile Lys Cys His Ser Met
                245                 250                 255

Lys Asp Leu Pro Glu Ser Asp Asp Ala Ile Ala Gln Trp Cys Arg Asp
            260                 265                 270

Gln Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Ile Ala Ala Asp
        275                 280                 285

Thr Phe Pro Gly Gln Gln Glu Gln Asn Ile Gly Arg Pro Ile Lys Ser
    290                 295                 300

Leu Ala Val Val Leu Ser Trp Ala Cys Val Leu Thr Leu Gly Ala Ile
305                 310                 315                 320

Lys Phe Leu His Trp Ala Gln Leu Phe Ser Ser Trp Lys Gly Ile Thr
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          325                    330                    335
Ile Ser Ala Leu Gly Leu Gly Ile Ile Thr Leu Cys Met Gln Ile Leu
          340                    345                350
Ile Arg Ser Ser Gln Ser Glu Arg Ser Thr Pro Ala Lys Val Val Pro
     355                     360                365
Ala Lys Pro Lys Asp Asn His His Pro Glu Ser Ser Ser Gln Thr Glu
     370                   375                380
Thr Glu Lys Glu Lys
385
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<211> 269
<212> DNA
<213> Glycine max

<400> 24
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ataagggtct acttcaacct ccctctccca gaacncattg tccgctacac ctacgagatg 120
ctcggcatca acctcgtcat ccgcggccac cgccctcctc cgccttcccc cggcaccccc 180
ggcaacctct acgtctgcaa ccaccgcacc gctctcgacc ccatcgtcat cgccattgcc 240
ctcggccgca aggtctcctg cgtcaccta                                   269

<210> 25
<211> 242
<212> DNA
<213> Glycine max

<400> 25
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tcacgtggct cccccttcggc ttcatcctct ccatcataag ggtctacttc aaccttcctc 120
tcccagaacg cattgtccgc tacacctacg agatgctcgg catcaacctc gtcatccgcg 180
gccaccgccc tcctccgcct tcccccggca ccccggcaa cctctacgtc tgcaaccacc 240
gc                                                               242

<210> 26
<211> 272
<212> DNA
<213> Glycine max

<400> 26
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ggtataacta taagctatta ggaatcagag ttattgtgaa gggtacccct ccaccacccc 180
caaagaaggg tcaaagtggt gtcctatttg tttgtaacca ccgcacagtt ttagaccctg 240
tggttactgc agttgcactt ggaagaaaaa tt                               272

<210> 27
<211> 218
<212> DNA
<213> Glycine max

<400> 27
atagcacagg agggttacat ggtgcctccg agcaaatcag caaaggcagt cccacaggag  60
cgtctgaaga gcagaatgat cttccacgac gggcgtttcg tgcagaggcc agacccaatg 120
aatgccctca tcaccttcac atggctccct ttgggtttcg tcctctccat cataagggtc 180
tacttcaacc tccctctccc agaacgcatc gtccgcta                         218

<210> 28
<211> 270
<212> DNA
<213> Glycine max

<400> 28
gtgcctgttg ctgtgaactg caagcagaac atgttctttg gaaccaccgt tcgtggcgtc  60
aagttctggg acccttaact tacttcttac atgaacccta ggcctgtgta cgaggttacc 120
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ttaccttgat accttgccg aggagatgtc ggttaaggct gggggaagt cgtccattga 180
ggtggccaac cacgtggcag aaggtgctgg gggatgtgtt agggtttgag tgcaccgggt 240
tgactaggaa ggataagtat atgttgttgg                                  270
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<210> 29
<211> 252
<212> DNA
<213> Glycine max

<400> 29
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agaattgttg gtacaactac aagctcttag gaatcagagt tattgtgaag ggtacccctc 180
caccgccccc aaagaagggt caaagtggtg tctatttgtt tgtaaccacc gcacagtatt 240
agaccctgtt gt                                                     252
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<210> 30
<211> 272
<212> DNA
<213> Glycine max

<400> 30
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tgttgctgca aagacaaatg caccagtagt accaattacc cttattggaa ctggtcaaat 180
catgcctgca ggaaaggagg gaatagtgaa cataggttct gtgaaagtgg ttatacataa 240
acctattgtt ggaaaggatc ctgacatgtt at                               272
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<210> 31
<211> 239
<212> DNA
<213> Glycine max

<400> 31
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gaagctcatc agaatgagtc tgctccatta atgatgttat ttccagaagg tacaaccaca 120
aatggagagt tcctccttcc attcaagact ggtggttttt tggcaaaggc accggtactt 180
cctgtgatat tacgatatca ttaccagaga tttagccctg cctgggattc catatctgg  239
```

<210> 32
<211> 242
<212> DNA
<213> Glycine max

<400> 32
```
gaacggcaac ggcaacagcg ttcgcgatga ccgtcctctg ctgaagccgg agcctccggt 60
cttccgccga cagcatcgcc gatatggaga agaagttcgc cgcttacgtc cgccgctacg 120
tgtacggcac catgggacgc ggcgagttgc ctcccaagga gaagctcttg ctcggtttcg 180
cgttggtcac tcttctcccc attcgagtcg ttctcgccgt caccatattg ctctttatt 240
ac                                                               242
```

<210> 33
<211> 248
<212> DNA
<213> Glycine max

<400> 33
```
ttcttcttct ctcactctct aaaaccctaa ctctatacat ggaagggaaa nctcaaatct 60
natgactaat taattaatcc atcgatcaag catggagtcc gaactcaaag acctcaattc 120
gaagccgccg aacggcaacg gcaacagcgt cgcgatgac cgtcctctgc tgaagccgga 180
gcctccggtc tccgccgaca gcatcgccga tatggagaag aagttcgccg cttacgtccg 240
ccgcgacg                                                         248
```

<210> 34
<211> 217
<212> DNA
<213> Glycine max

<400> 34
```
aaaaccctaa ttctatacat ggaagggaaa tctcaaatct aatgactaat taattaatcc 60
```

```
atcgatcaag catggagtcc gaactcaaag acctcaattc gaagccgccg aacggcaacg 120
gcaacagcgt tcgcgatgac cgtcctctgc tgaagccgga gcctccggtc tccgccgaca 180
gcatcgccga tatggagaag aagttcgccg cttacgt                         217
```

<210> 35
<211> 257
<212> DNA
<213> Glycine max

<400> 35
```
atctctgtct ctgcatttcc ctccctaaaa ccctaattct acatttggaa aggaaatctc 60
aaatctaatg actaattaat caatcaatcg tattaataat ccatcgatca agtatggagt 120
ccgaactcaa agacctcaat tcgaagccac ccaactgcaa cggcaacgcc aacagcgttt 180
gcgacgaccg tcctctgctg aagccggagc ctccggcctc ctccgacagc atcgccgaga 240
tggagaagaa gttcgcc                                               257
```

<210> 36
<211> 284
<212> DNA
<213> Glycine max

<400> 36
```
cccgaccaaa acaggttttt gtggccaatc atacttccat gattgatttc attatcttag 60
aacagatgac tgcatttgct gttattatgc agaagcatcc tggatgggtt ggattattgc 120
agagcaccat tntggagagt gtagggtgta tctggttcaa ccgtacagag gcaaaggatc 180
gagaagttgt ggcaaggaaa ttgagggatc atgtcctggg agctaacaac aaccctcttc 240
ttatatttcc tgaaggaact tgtgtaaata atcactactc gtca                284
```

<210> 37
<211> 246
<212> DNA
<213> Glycine max

<400> 37
```
ggagatccgc ataagcaaat caatcatcct gttccttcct tatctctgtc tctgcatttc 60
cctccctaaa accctaattc tacatttgga aaggaantct caaatctaat gataattaat 120
caatcaatcg tattaataat ccatcgatca agtatggagt ccgaactcaa agacctcaat 180
tcgaagccac ccaactgcaa cggcaacgcc aacagcgttt gcgacgaccg tcctctgctg 240
aagccg                                                          246
```

<210> 38
<211> 278
<212> DNA
<213> Glycine max

<400> 38
```
gttttctatt gccacgttgt ggaagcgtaa cgaagatgaa tggcattggg aaactcaaat 60
cgtcgagttc tgaattggac cttcacattg aagattacct accttctgga tccagtgttc 120
aacaagaacg gcatggcaag ctccgactgt gtgatttgct agacatttct cctagtctat 180
ctgaggcagc acgtgccatt gtagatgata cattcacaag gtgcttcaag caaatcctcc 240
agaaccttgg aactggaatg tttatttgtt cctttgt                        278
```

<210> 39
<211> 312
<212> DNA
<213> Glycine max

<400> 39
```
ttaactttgg cacattctcc ttttgttcat caatgtgtgt tgtaaattgt ncatttcctt 60
cagaggtctt tggtaganat gatgtgcagt ttctgtggtg catcttggac tgnggntgtt 120
aagnatcatg gacccaggcc tagcaggaga ccaaagcagg tttttgtagc caaccatact 180
tcatgattga tntcattatn tnagaacaga tgactgcttt tgcngttatn atgcagaagc 240
atcctggatg ggttggtaag cntacagnat gtcaacngtg tatnaaatat gntacacnnn 300
acttgcgtct tc                                                    312
```

<210> 40
<211> 255
<212> DNA
<213> Glycine max

```
<400> 40
ggattattgn ngcanatgca gtcatctgtt ctaagataat ganatcnatc atggaagtat 60
gattggncac anaaacctgt yttttggttg gatactaggt cttggcccat ggtacttgac 120
naccccagtc catgatgcaa canaganact gnacatcatc tccaccaaac ccctctgana 180
ganacgagaa ttgagcaatt tagagtacct tggtttgatg caagtcagta tattcaagtt 240
tctattcatc aaagg                                                 255


<210> 41
<211> 291
<212> DNA
<213> Glycine max


<400> 41
caacctccca tgcaatcgct caccctctcc gtcacctgaa tctgtttttct attccctccg 60
tcgcgtaaca aggatgaatg gcattgggaa actcaaatcg tcgagttctg aattggacct 120
tcacattgaa gattacctgc cttctggatc cagtgttcaa caagaacggc atggcaagct 180
ccgcctgtgt gatttgctag acatttctcc tagtctatct gaggcagcac gtgccattgt 240
agatgataca ttcacaaggt gcttcaagtc aaatcctcca gaaccttgga a           291


<210> 42
<211> 284
<212> DNA
<213> Glycine max


<400> 42
ctgcaaccta ccatgcaatt cctcacctga atccgttttc tattgccacg ttgtggaagc 60
gtaacgaaga tgaatggcat tgggaaactc aaatcgtcga gttctgaatt ggaccttcac 120
attgaagatt acctaccttc tggatccagt gttcaacaag aacggcatgg caagctccga 180
ctgtgtgatt tgctagacat ttctcctagt ctatctgagg cagcacgtgc catgtagatg 240
atacatcaca aggtgctcaa gtcaaatctc cagaaccttg gaat                  284


<210> 43
<211> 268
<212> DNA
<213> Glycine max


<400> 43
ctgaagtatt ctcgtcctag cccaaagcat agagaaaggn agcaacagaa ctttgctgag 60
tcagtgctgc ggcgatggga ggaaaagtga tgtgtacctt tatgtggtgt tgttcttaat 120
tattcttagt aatgccattg cttcgacccc ttttttttgct tttgttttgt cattgctaac 180
tatttatttt taacactttt attaaagata tggcatatat ncacttcagt anacaaagtt 240
gtnccagtaa tttnttttcc aaaaaaaa                                    268


<210> 44
<211> 241
<212> DNA
<213> Glycine max


<400> 44
gancaaaatt gccctccatc actttccttg ttagagttgg tttctgcnac ctaccatgca 60
attccctcac ctgaatccgt tttctattgc cacgttgtgg aagcgtaacg aagatgaatg 120
gcattgggaa actcaaatcg tcgagttctg aattggacct tcacattgaa gattacctac 180
cttctggatc cagtgttcaa caagaacggc atggcaagct ccgactgtgt gatttgctag 240
a                                                                241


<210> 45
<211> 247
<212> DNA
<213> Glycine max


<400> 45
gtaggatgtc tgagatcctt gccccaatca aaacggtgcg gttaactaga aaccgcgacg 60
aggatgcgaa aatgatgaaa aatttgctgg ggcaagggga cctggtggtt tgtcctgaag 120
ggaccacatg tagagaacct tatttattga ggttcagccc tctgttctca gagatgtgcg 180
atgagattgt ccccgttggc agttgattcc cagttatatg ttccacggaa ccactgctgg 240
tgganta                                                          247


<210> 46
<211> 271
<212> DNA
```

```
<213> Glycine max

<400> 46
tgcaggggggg cttgttagag ccatagtttt ggttcttcta tacccttttg tttgtgtcgt   60
aggaaaagag atggggttga agataatggt catggcatgc ttcttcggga tcaaagcatc  120
gagcttcaga gttggaaggt ccgttttgcc cnaattcttc tnggaggacg ttngtgcaga  180
aatgtttgag gcactcaaaa aaggagggaa gacagtggga gttaccaatt taccccacgt  240
gatggtggaa agcttcttga gagagtattt g                                  271


<210> 47
<211> 242
<212> DNA
<213> Glycine max

<400> 47
ttcacagctg tcacgccgtn aacggaaaat ggcaacggcg agacgcagtt tcccgcctat   60
caccgaatgc aacggaacga cnccgtgcga ntctgtngnc gccgacctcg agggtacgct  120
cctcatctcc cgtngctcgt tcccgtactt catgctcgtc gccgtcgaag ccggcagcnt  180
cctccgcggc ctcatgctnc tcctctccct tccgttcgtc atnatcgcct acctcttcat  240
ct                                                                 242


<210> 48
<211> 244
<212> DNA
<213> Glycine max

<400> 48
acatattctt cagttagctc ccccaaccta tacacttcac caccacacca caaccctacc   60
ctctctctct gtcatggtca ttggaggagc cttccctcgt ttcgacccaa tcaccaaatg  120
tagacccaag accgctccaa ccagaccatc gcctcggacc tcgatggcac cctccttgtc  180
tcccggagtg ccttccccta ctacttcctc gtcgccctcg aagccggcag cgtcttccga  240
gcct                                                               244


<210> 49
<211> 230
<212> DNA
<213> Glycine max

<400> 49
caacattcca cctagctccc caatcacatc ttcaccacac cataaacctt cttaatttct   60
ctcttcattt tctcctctat tgtcataatc atggggacct tccctcgctt cgacccaatc  120
accacccaag accggtccaa ccagaccgtg gcctccgacc ttgacggcac cctcctcgtc  180
tcccggagcg ccttccccta ctacctcctc gttgccctcg aagccggcag            230


<210> 50
<211> 265
<212> DNA
<213> Glycine max

<400> 50
ctggtgaata atcctaagtt atggagtctg tggtgtgtga gctagaaggc acgcttgtga   60
aggacaagga tgcgttctca tacttcatgt tggttgcgtt tgaagcttca ggtttggttc  120
gtttcgcctt gttgctaaca ctattgcccg tgattcggtt ccttgacatg gttggcatga  180
acgatgcatc tctcaagcta ntnatcttcg tggctgtggc tggtgttcca aagtccgaga  240
ttgaatcagt ggctagggca gtttt                                        265


<210> 51
<211> 252
<212> DNA
<213> Glycine max

<400> 51
ctggtgaata atcctaagtt atggagtctg tggtgtgtga gctagaaggc acgcttgtga   60
aggacaagga tgcgttctca tacttcatgt tggttgcgtt tgaagcttca ggtttggttc  120
gtttcgcctt gttgctaaca ctattgcccg tgattcggtt ccttgacatg gttggcatga  180
acgatgcatc tctcaagcta atgatcttcg tggctgtggc tgggttccaa agtccgagat  240
tgaatcagtg gc                                                      252


<210> 52
<211> 218
```

```
<212> DNA
<213> Glycine max

<400> 52
aactgcaact acaacaacat tcattcattc acagctgtca cgccgtgaac ggaaaatggc 60
aacggcgaga cgcagtttac ccgcctatac accgaatgca acggaacgac accgtgcgag 120
tctgtggccg ccgacctcga cggtacgctc ctcatntccc gtagctcgtt cccgtacttc 180
atgctcgtcg ccgtcgaagc cggcagcctc ctccgcgg                        218

<210> 53
<211> 262
<212> DNA
<213> Glycine max

<400> 53
ggttaaggac attgagatgg tcgnntcctc ggtgctgccc aagttctaca ccgaggacgt 60
gcnccccgag agctggagag tcttcaatcc ttcgggaagc gttacattgt cactgctagt 120
ctagggtgat ggtggagcan tttgttaaga cgtttcttgg ggctgataag gtgcttggga 180
ctgagcttga ggccacgaaa tcggggaggt tcatgggttt gttaaggagc ctggtgtgct 240
tgttggggag cacaagaaag tg                                         262

<210> 54
<211> 212
<212> DNA
<213> Glycine max

<400> 54
gcaactacaa caacattcat tcattcacag ctgtcacgcc gtgaacggaa aatggcaacg 60
gcgagacgca gtttcccgcc tatcaccgaa tgcaacggaa cgacgccgtg cgagtctgtg 120
gccgccgacc tcgacggtac gctcctcatc tcccgtagnc cgttcccgta cttcatgctc 180
gtngccgtcg aagccggcag cctcctccgc gg                              212

<210> 55
<211> 273
<212> DNA
<213> Glycine max

<400> 55
catggttttc ttgagcttct ttggcctcag aaaggacaca ttcagaacag gatcagctgt 60
tctggcaaag ttcttcttag aagatgttgg attggaaggc tttgaggccg taatatgttg 120
tgagagaaaa gttggcatcta gtaagttgcc aagggtcatg gttgaaaatt tcctcaagga 180
ctatttaggg gttgatgctg ttatagcaag agaattgaag tcctttagtg gcttcttttt 240
gggagttttt gagagtaaga agccaattaa aat                             273

<210> 56
<211> 257
<212> DNA
<213> Glycine max

<400> 56
ctctcaaaaa aggagggaag acagtgggag tcaccaatct accccatgtg atggtggaaa 60
gcttcttgag agagtatttg gacattgatt tcgttgtggg cagggagctg aaagttttct 120
gtggatacta cgtaggattg atggatgaca caaaaactat gcatgccttg gagctggtta 180
aagaaggaaa aggatgctcc gacatgatcg gaatcacaag gtttcgcaac atacgcgacc 240
atgatgattt tttctcc                                               257

<210> 57
<211> 240
<212> DNA
<213> Glycine max

<400> 57
gaactaagtg tgaaccacta ccaagaaaca agcttttaag tccaattatt tttcatgagg 60
gtaggtttgc tcaaaggcca actcctctag ctgnnctctt gaccttccta tggctgccaa 120
ttggcatcat actctccatc ttaagggtct accttaacat ccctttgcct gaaagaattg 180
cttggtacaa ctacaagctc ttaggaatca gagttattgt gaagggtacc cctccaccgc 240

<210> 58
<211> 254
<212> DNA
```

<213> Glycine max

<400> 58
cttggaataa gggtcattag gaagggtatc cctccacccc cagcnaagaa gggccaaagt 60
ggagtcctat ttgtatgcaa ccacaggaca gttttagacc ctgtggttac agctgttgca 120
ttaggaagga aaattagctg tgtcacatat agcataagca aattcactga aataatttca 180
ccaatcaaag ctgtggcact ctctagggag agggacaaag atgctgccaa catcaagang 240
ttgcttgagg aagg   254

<210> 59
<211> 267
<212> DNA
<213> Glycine max

<400> 59
gccaganaga cttgcttggt acaactacaa gcttcttgga ataagggtca ttaggaaggg 60
tatccctcca cccccagcaa agaagggcca aagtggagtc ctatttgtat gcaaccacag 120
gacagtttta gaccctgtgg ttacagctgt tgcattagga aggaaaatta gctgtgtcac 180
atatagcata agcaaattca ctgaaataat tcaccaatca aagctgtggc actctctagg 240
gagagggacc nagatgctgc cnacatc   267

<210> 60
<211> 261
<212> DNA
<213> Glycine max

<400> 60
gtaaccacag ggtctaaaac tgtgcggtgg ttactgcagt tgcacttgnc nagaaaaatt 60
tgcttatgct atatgtgaca cagctaattc actgnaataa tttcaccaat taaagctgtg 120
gcactctcaa ggganngaga gaaagatgct gccaatatcc ngagactact tgaggaaggg 180
gacttggtga tttgccctga aggcacaact tgtagagagc cttcctcttg aggttcagtg 240
cactatttgc tgaactcact g   261

<210> 61
<211> 258
<212> DNA
<213> Glycine max

<400> 61
caaggagctc acatgcagtg gagggaaatc agctattgaa gttgcaaact acattcaaag 60
ggttcttgca gggactttgg gatttgagtg cacaaatttg actaggaaga gcaaatatgc 120
catgcttgca ggcacagatg ggacagttcc atctaaggag aaggcttgan aagggagaga 180
aattaagttc tcccttttga ttattctgta ttggtgccca atgtgtttcc aaaacactta 240
gaattatgat agaaataa   258

<210> 62
<211> 258
<212> DNA
<213> Glycine max

<400> 62
attggcataa tcctctccat cctaagggtc tatctcaaca tccctctgcc agaaagactt 60
gcttgntaca actacaagct tcttggaata agggtcatta ggaagggtat ccctccaccc 120
ccagcaaaga agggccaaag tggagcctat ttgtatgcaa ccacaggaca gttttagacc 180
ctgtggttac agctgttgca ttaggaagga aaattagctg tgtcacatat agcataagca 240
aattcactga aataattt   258

<210> 63
<211> 239
<212> DNA
<213> Glycine max

<400> 63
cacttcacca ccacaccaca accctaccct ctctctctgt catggtcatt ggaggagcct 60
tccctcgttt cgacccaatc accaaatgta gcacccaaga ccgctccaac cagaccatcg 120
cctcggacct cgatggcacc ctccttgtct cccggagtgc cttcccctac tacttcctcg 180
tcgccctcga agccggcagc gtcttccgag ccctccttct cttaaccttc gtccccttc 239

<210> 64
<211> 531

<212> DNA
<213> Glycine max

<400> 64
ccgagaaccg gtctaaccaa accgtggcct cggacttgga cggcaccctc ctggtgtccc 60
ccagcgcatt tccttactac atgctggtcg ccatcgaagc cggcagcttc ctccgtggcc 120
ttgtcctcct tgcctccgtc cctttcgtgt attcacgtac atattcctct ccgagaccgc 180
ggccatcaag tccctgatct tcatcgcctt cgcgggcctg aaggtcaggg acgttgagat 240
ggtcgcgtgc tcggtgctgc ccaagttcta cgccgacata ttcttcagtt agctccccca 300
acctatacac ttcaccacca caccacaacc ctaccctctc tctctgtcat ggtcattgga 360
ggagccttcc ctcgtttcga cccaatcacc aaatgtagca cccaagaccg ctccaaccag 420
accatcgcct cggacctcga tggcaccctc cttgtctccc ggagtgcctt cccctactac 480
ttcctcgtcg ccctcgaagc cggcagcgtc ttccgagccc tccttctctt a   531

<210> 65
<211> 256
<212> DNA
<213> Glycine max

<400> 65
acatattctt cagttagctc ccccaaccta tacacttcac caccacacca caaccctacc 60
ctctctctct gtcatggtca ttggaggagc cttccctcgt ttcgacccaa tcaccaaatg 120
tagcacccaa gaccgctcca accagaccat cgcctcggac ctcgatggca ccctccttgt 180
ctcccggagt gccttcccct actacttcct cgtcgccctc gaagccggca gcgtcttccg 240
agccctcctt ctctta   256

<210> 66
<211> 260
<212> DNA
<213> Glycine max

<400> 66
ccatccaaca tattcttcag ttagctcccc caacctatac acttcaccac cacaccacaa 60
ccctaccctc tctctctgtc atggtcattg gaggagcctt ccctcgtttc gacccaatca 120
ccaaatgtag cacccaagac cgctccaacc agactatcgc ctcggacctc gatggcaccc 180
tccttgtctc ccggagtgcc ttcccctact acttcctcgt cgccctcgaa gccggcagcg 240
tcttccgagc cctccttctc   260

<210> 67
<211> 248
<212> DNA
<213> Glycine max

<400> 67
caccaaccaa acctcactct ccctttctcc cctgaccctc tccctgccat ggtcatggga 60
gcctttggcc acttcgaacc ggtctccaaa tgcagcaccg agaaccggtc taaccaaacc 120
gtggcctcgg acttggacgg caccctcctg gtgtcccccca gcgcatttcc ttactacatg 180
ctgggcgcca tcgaagccgg cagcttcctc cgtggccttg tcctccttgc ctccgtccct 240
ttcgtgta   248

<210> 68
<211> 283
<212> DNA
<213> Glycine max

<400> 68
ttcttcccca ccatcacacc aancaaacct cactctncct ggccatggtc atgnnngcct 60
ttccgccact tcgaaccggt ttccaaatgc agcaccgaaa accggtttaa ccaaaccgtg 120
gcctcggact tggacggcac cctcctggtg tcccctagcg cctttcctta ctacatgctc 180
gtcgccatcg aagccggcag cttcctccgt ggccttgtcc tccttggatc cgtcccttтc 240
gtgtacttca cgtacatatt cttctccgag accgcggcca tca   283

<210> 69
<211> 258
<212> DNA
<213> Glycine max

<400> 69
ctcttcttcc ccaccatcnn accaaccaaa cctcactctc cctgaccatg gtcatgggag 60
cctttcgcca cttcgaaccg gtttccaaat gcagcaccga aaaccggttt aaccaaaccg 120

```
tggcctcgga cttggacggc accctcctgg tgtcccctag cgcctttcct tactacatgc 180
tcgtcgccat cgaagccggc agcttcctcc gtggccttgt cctccttgga tccgtccctt 240
tcgtgtactt cacgtaca                                                258
```

<210> 70
<211> 256
<212> DNA
<213> Glycine max

<400> 70
```
tgcaactaca acaacattca ttcattcaca gctgtcacgc cgtgaacgga aaatggcaac 60
ggcgagacgc agtttcccgc ctatcaccga atgcaacgga acgacaccgt gcgagtctgt 120
ggccgccgac ctcgacggta cgctcctcat ctcccgtagc tcgttcccgt acttcatgct 180
cgtcgccgtc gaagccggca gcntcctccg cggcctcatc ctcctcctng ccantccgtt 240
cgtcatcanc gcctac                                                 256
```

<210> 71
<211> 259
<212> DNA
<213> Glycine max

<400> 71
```
cttccccacc atcacaccan ggcnaacctc antctccctt tctccacnga ccctctccct 60
gccatngtca tggggancctt tggccacttc gaaccggtct ccaaatgcag caccgagaac 120
cggnctaacc aaaccgtggc ctcggacttg dacggcaccc tcctggtgtc ccncagcgca 180
tttccttact acatgctggc ngccatcgaa gccggcagct tcctccgtgg ccttgtcctc 240
cttgcctccg tccctttcg                                               259
```

<210> 72
<211> 249
<212> DNA
<213> Glycine max

<400> 72
```
ccaacatatt cttcagttag ctcccccaac ctatacactt caccaccaca ccacaaccct 60
accctctctc tctgtcatgg tcattggagg agccttccct cgtttcgacc caatcaccaa 120
atgtagcacc caagaccgct ccaaccagac catcgcctcg gacctcgatg gcaccctnct 180
tgtctcccgg agtgccttcc cctactactt cctcgtcgcc ctcgaagccg gcagcgtctt 240
ncgagccct                                                         249
```

<210> 73
<211> 257
<212> DNA
<213> Glycine max

<400> 73
```
caaccctctt cttccccacc atcacaccaa ncaaacctca ctctcccttt ctcccctgac 60
cctctccctg ccatggtcat gggagccttt ggccacttcg aaccggtctc caaatgcagc 120
accgagaacc ggtctaacca aaccgtggcc tcggacttgg acggcaccct cctggtgtcc 180
cccagcgcat ntccttacta catgctggtc gccatcgaag ccggcagctt cctccgtggc 240
cttgtcctcc ttgcctg                                                257
```

<210> 74
<211> 255
<212> DNA
<213> Glycine max

<400> 74
```
gccgaagacg tgcaccggga gagttggaga gtgttcaact ctttcgggaa gcgttacatt 60
gtcacggcta gtcctagggt gatggtggag ccgtttgtta aggcgtttct cggggctgac 120
aaggtgcttg ggactgaact tgaggccacc aaatcgggga cgttcactgg gtttgttaag 180
aagcctggtg tgcttgttgg ggagcataag aaagtggctc tggtgaagga gtttcagggt 240
aattacctga cttgg                                                  255
```

<210> 75
<211> 244
<212> DNA
<213> Glycine max

<400> 75
```
```

```
caacaacatt cattcattca cagctgtcac gccgtgaacg gaaaatggca acggcgagac 60
gcagtttccc gcctatcacc gaatgcaacg gaacgacacc gtgcgagtct gtggccgccg 120
acctcgacgg tacgctcctc atcncccgta gctcgttccc gtacttcatg ctcgtcgccg 180
tcgaagccgg cagcctcctc cgcggcctca tgcnttcctg ggtttanttt gagnacccct 240
gagg                                                          244
```

<210> 76
<211> 240
<212> DNA
<213> Glycine max

<400> 76
```
gctggctacc ctcttcttcc ccaccatcac accaatcaaa cctcactcta ccctggccat 60
ggtcatggga gcctttncgc cacttcgaac cggtttccaa atgcagcacc gaanaccggt 120
ttnaccanac cgtggcctcg gncttggacg gcaccctcct ggtgtcccct agcgcctttc 180
cttactacat gctcgtcgcc atcgaagccg gcagcttcct ccgtggcttg tcctccttgg 240
```

<210> 77
<211> 263
<212> DNA
<213> Glycine max

<400> 77
```
gtttctcggg gctgacaagg tgcttgggac tgaacttgag gccaccaaat cggggacgtt 60
cactgggttt gttaagaagc ctggtgtgct tgttggggag cataagaaag tggctctggt 120
gaaggagttt cagggtaatt tacctgactt gggtctaggt gatagtaaaa gtgattatga 180
cttcatgtca atttgcaagg aagggtacat ggtgccaaga actaagtgtg aaccactacc 240
aagaaacaag cttttaagtc caa                                      263
```

<210> 78
<211> 258
<212> DNA
<213> Glycine max

<400> 78
```
ggccacgaaa tcggggaggt tcactgggtt tgttaaggag cctggtgtgc ttgttgggga 60
gcacaagaaa gtggctgttg tgaaggagtt tcagggtaat ttacctgact tgggactagg 120
agatagtaaa agtgattatg acttcatgtc aatttgcaag gaagggtaca tggtgccaag 180
gactaagtgt gaaccactac caagaaacaa actttttaagt ccaattattt ntcatgaggg 240
taggtttgtt caaaggcc                                            258
```

<210> 79
<211> 260
<212> DNA
<213> Glycine max

<400> 79
```
ctcttcttcc ccaccatcac accaancaaa cctcactctc cctttctccc ctgaccctct 60
ccctgccatg gtcatgggag cctttggcca cttcgaaccg gtctccaaat gcagcaccga 120
gaaccggtct aaccaaaccg tggcctcgga cttggacggc accctcctgg tgtcccccag 180
cgcatttcct tactacatgc tggtcgccat cgaagccggc agcttcctcc gtgggccttg 240
tcctccttgc ctccgtccct                                          260
```

<210> 80
<211> 257
<212> DNA
<213> Glycine max

<400> 80
```
gggaacaaca acaaatggca ngaaccttat ctccttccaa cttggtgcat ttatccctgg 60
atacccaatc cagcctgtaa ttgtacgcta tcctcatgtg cactttgacc aatcctgggg 120
tcatgtntct ttgggaaagc ttatgttcag aatgttcact caatttcaca acttttttga 180
ggtagaatat cttcctgtca tttatcccct ggatgataag gaaactgctg tancttntcg 240
ggagaggact agccggg                                            257
```

<210> 81
<211> 272
<212> DNA
<213> Glycine max

```
<400> 81
catacctttt gttggcacca ttattagagc aatgcaggtc atatatgtta acagattctt 60
accatcatca aggaagcagg ctgttaggga aataaaggaa ctgaataaca gagaagggcc 120
tcttgtgata aatttcctcg agtactatta tttcccgagg gaacaacaac taatggcagg 180
aaccttatct ccttccaact tggtgcattt atccctggat acccaatcca gcctgtaatt 240
atacgctatc ctcatgtaca ctttgaccaa tc                                272


<210> 82
<211> 245
<212> DNA
<213> Glycine max


<400> 82
gggcatttca catactagag ttcatcccag tgaaaagaaa gtgggaggct gatgaatcaa 60
tcatgcgcca tatgctttct acattcaagg atccacaaga tcctctctgg cttgcgcttt 120
tcccagaagg cactgatttc actgagcaaa agtgccttcg gagtcaaaaa tatgctgctg 180
aacataagtt accggttctg aaaaatgttt tacttccaag gacaaagggg cttctgtgcc 240
gcttg                                                              245


<210> 83
<211> 268
<212> DNA
<213> Glycine max


<400> 83
cagtgtcctt cctttctgga caatgttttt ggtgttgacc cttcagaagt gcacctgcat 60
gtgcggcgta ttccggtgga ggagattcca gcttctgaaa ccaaagctgc ttcttggtta 120
atcgacacat tccagatcaa ggaccaattg ctttcggatt tcaagattca aggccatttc 180
cctaaccaac taaatgaaaa tgaaatttct agatttaaga gcctactctc ttttatggtg 240
atagtttctt ttactgccat gtttattt                                     268


<210> 84
<211> 265
<212> DNA
<213> Glycine max


<400> 84
gaaagagact gggcaaaaga tgaaacatca ctgaagtcag gttttaggca tctagagcac 60
atgccattcc ctttctggtt ggcccttttt gttgaaggaa ctcgtttcac gcagacaaag 120
cttttacaag ctcaagagtt tgctgcttca aaagggctgc ctatacctag aaatgttttg 180
attcctcgta ctaagggttt tgtcacagca gnacaaagcc ttcggccatt tcgttccagc 240
catttatgat tgcacatatg cagtt                                        265


<210> 85
<211> 265
<212> DNA
<213> Glycine max


<400> 85
gaaagagact gggcaaaaga tgaaacatca ctgaagtcag gttttaggca tctagagcac 60
atgccattcc ctttctggtt ggcccttttt gttgaaggaa ctcgtttcac gcagacaaag 120
cttttacaag ctcaagagtt tgctgcttca aaagggctgc ctatacctag aaatgttttg 180
attcctcgta ctaagggttt tgtcacagca gnacaaagcc ttcggccatt tcgttccagc 240
catttatgat tgcacatatg cagtt                                        265


<210> 86
<211> 301
<212> DNA
<213> Zea mays


<400> 86
ctcgtcgtca agggcacccc gccgccgccg cccaagaagg gccacccggg cgtcctcttc 60
gtctgcaacc accgcaccgt gctcgacccc gtcgaggtgg ccgtggcgct cgccgcaag 120
gtcagctgcg tcacctacag catctccaag ttctccgagc tcatctcgcc catcaaggcc 180
gtcgcgctgt cgcggggggc gacaaggacg ccgagaacat ccgccgcctg ctggaggagg 240
gcgacctggt catctgcccc gagggnaaca actgccgcga gcccttcctg ctgcgttcag 300
g                                                                  301


<210> 87
<211> 309
```

```
<212> DNA
<213> Zea mays

<400> 87
cgctcatgcg gtgtacatca acctgccgct gcccgagcgc atcgtctact acacctacaa  60
gctcatgggc atcaggctcg tcgtcaaggg caccccgccg ccgccgccca agaagggcca 120
cccgggcgtc ctcttcgtct gcaaccaccg caccgtgctc gaccccgtcg aggtggccgt 180
ggcgctgcgc cgcaaggtca gctgcgtcac ctacagcatc tccaagttct ccgagctcat 240
ctcgcccatc aaggccgtcg cgctgtcggg gaggcgacaa ggacgccgag aacatccgcc 300
gcctgctgg                                                         309


<210> 88
<211> 304
<212> DNA
<213> Zea mays

<400> 88
tggctgtgca ggaggcctac ctggtgacgt caaggaagta cagcccggtg cccaggaacc  60
agctgctgag cccgctgatt cgtgcacgac ggccgcctcg tgcagcgccc gacgccgctc 120
gtcgcgctcg tcaccttcct ctggatgccg ttcggcttcg cgctggcgct catgcgcgtg 180
tacatcaacc tgccgctgcc cgagcgcatc gtctactaca cctacaagct catgggcatc 240
aggctcgtcg tcaagggcac cccgccgccg ccgcccaaga agggccaccc gggcgtcctc 300
ttcg                                                              304


<210> 89
<211> 312
<212> DNA
<213> Zea mays

<400> 89
ggttcatcca cttgtgttgc tattngaccg gtaccgtagg agagcacagc actancatcg  60
caaagatttn gggctacggt gacaatctcc atgttctaca atcttnaggt cgaaggaatg 120
gagaatctgc ctccaaatag ctgtcctggt gtctatgttg ctaaccatca gagcttcttg 180
gatatttata cccttctaac tctagggagg tgcttcaaat ttataagcaa gaccagcatc 240
tttatgttcc ctattatagg gtgggcaatg tatctcttgg gtgtgattcc tctgcggcgt 300
atggacagca gg                                                     312


<210> 90
<211> 264
<212> DNA
<213> Zea mays

<400> 90
ggtgctgtat ctgaaagaat ccatcgtgct catcaacaga aaaatgcacc aatgatgcta  60
ctcttcccct gagggcacaa ctacaaatgg ggattatctc cttccattca aaacaggtgc 120
ttttcttgca aaggcaccag ttcaaccagt cattttgaga tatccttaca aaagatttaa 180
tgcagcatgg gattccatgt caggggcacg tcatgtattt ctgctgctct gtcaatttgt 240
aaattaccta gaggtggtcc gctt                                         264


<210> 91
<211> 212
<212> DNA
<213> Zea mays

<400> 91
aaatgtcttg gatgcatttt tgttcagcgg gagtcgaaaa caccagattt caaaggtgtt  60
tcaggtgctg tatttgaaag aatccatcgt gctcatcaac agaaaaatgc accaatgatg 120
ctactcttcc ctgagggcac aactacaaat ggggattatc ccttccatt caaaacaggt 180
gctttncttg caaaggcacc agttcaacca gt                                212


<210> 92
<211> 267
<212> DNA
<213> Zea mays

<400> 92
gtctaaagaa atngaaaggc gtggggnaat tgtgtctaat catgtntctt atgtggatat  60
tctttatcan atgtcagcct cttttcctag ttttgttgct aagagatcag tggntagatt 120
gcctctagtt ggtctcataa gcaaatgtct ggatgcatt tttgttcagc gggagtnnaa 180
aatncanatt tcaaaggtgt ttaaggtgtg gnatctgaaa gaatccatcg tgctcatcaa 240
```

```
cagaaaaatg caccaatgat gctactc                                      267
```

<210> 93
<211> 152
<212> DNA
<213> Zea mays

<400> 93
```
ctacaaatgg ggattacctt cttccattta agactggagc ctttnttgca ggtgcaccag  60
tgcagccagt cattttgaaa tacccttaca ggagatttag tccagcatgg gattcaatgg 120
atggagcacg tcatgtgtta ttgctgctct gt                               152
```

<210> 94
<211> 274
<212> DNA
<213> Zea mays

<400> 94
```
aaaatataaa ttaatatggt cttaatccca ccatataaat aacgttctct ttctgcaggg  60
caatttagtt ctttctaata ttgggctggc agagaagcgc gtgtaccatg cagcactgac 120
tggtagtagt ctacctggcg ctagacatga gaaagatgat tgaaagacgt tgcgtcgctt 180
tttctgtaac agacagccga ggaacactta aaaatgtaac tgtgtgcgtg tttttatacc 240
tgtaatgtgg cagtttattt gtttgaggag gctg                             274
```

<210> 95
<211> 295
<212> DNA
<213> Zea mays

<400> 95
```
aatagctatc aagtacaata aaatatttgt tgatgccttt tggaacagta agaagcaatc  60
ttttacaatg cacttggtcc ggctgatgac atcatgggct gttgtgtgtg atgtttggta 120
cttacctcct caatatctga gggaggagga gacggcaatt gcatttgctg agagagtaag 180
ggacatgata gctgctagag ctggactaaa gaaggttcct tgggatggct atctgaaaca 240
caaccgtcct agtcccaaac acactgaaga gaacaacgca tattgccgat ctgtc      295
```

<210> 96
<211> 273
<212> DNA
<213> Zea mays

<400> 96
```
gngccatctc accggcggcn ggcctgcggc cggcaaccgg aggcgatggc gagctngtct  60
gtggtggcgg acatggagca ntaccgcccc aacctggagg actacctccc gcccgactcg 120
ctcccgcagg aggcgcccag gaatctccat ctgcgcgatc tgcttgacat ctcgccggtg 180
ctaaccgagg cagcggggtgc catagtcgat gattcattca cccgttgctt taagtcgaat 240
tctccagaac catggaatgg aacatatatt tgt                              273
```

<210> 97
<211> 127
<212> DNA
<213> Zea mays

<400> 97
```
ctcaatatct ganggaggga gagactgcaa ttgcgtttgc tgagagagta agggacatga  60
tagcagctag agctggtctt aagaaggtcc cgtgggatgg ctatctgaag cacaaccgcc 120
ctagtcc                                                           127
```

<210> 98
<211> 286
<212> DNA
<213> Zea mays

<400> 98
```
gaaccgtacg cgcctcatta cgcccatcca cgtgctcgcc tctccccatc gcataatttt  60
nctcggcggc gtcgccatct ccancggcng cnggcctgcn gccggcaacc ggaggcgatg 120
gcgagctcgt ctgtggcggc ggacatggag ctggaccgcc ccaacctgga ggactacntc 180
ccgcccgant cgctcccgca ggaggcgacc aggaatctcc atctgngcga tctgcttgan 240
atctcgccgg tgctaaccga ggcagcgggt gccatagtcg atgatt               286
```

```
<210> 99
<211> 308
<212> DNA
<213> Zea mays

<400> 99
cgccatctca tcggcggcgg gcgtgcggcc ggcggcngag gcgaggngcg attggcgagc  60
tcgtctgtgg cgccggacat ggagctggac cgcccanacc tggaggacta nctcccgccc  120
gactcgnncc cgcagaggcg ccccggaatc tccanctgcg cgatctgctg gacatcncgc  180
cggtgctcac cgaggcagcg ggtgccattg tcgatgactc cttcacacgg ngctttaagt  240
caaattctcc agagccatgg aattggaaca tatatctgtt cccctattgt gctttggtgt  300
ataataag                                                            308


<210> 100
<211> 282
<212> DNA
<213> Zea mays

<400> 100
cagaaactag angttagtca cagcatggca ttaaattgtc atagtaaaca acancncact  60
gagcaactat gcaatttaat gccatgctgt gactaacttc tagtttctgg cattaaatta  120
ctgtttggct actaggaaga ccgaggtaga gaagcaaata taagaatacc ctccaacgca  180
canccaaatg acagagtaaa tgaaggtagg gttcaccttc ttgaacatga ccgtatactg  240
gttgttaaca caagttcctc tgggaaaatc agagagggtt tt                     282


<210> 101
<211> 282
<212> DNA
<213> Zea mays

<400> 101
ggcgcggctg gccgtggcgc tggtcctgcc gtacagtact cgacgccgat cctggcngcg  60
acnggcatgt cgtggcggct caaagggtng cgcccngngc ttgcnnngcc gtgctccggc  120
gggcgctgnc agctgttcgt gtgcaacnac cggacgctga tcgacccngt gtacgtgtcc  180
gtagcgtgga ccgggaaatg cgcgncgtgt nctacagnct gangcggntn tcggagctca  240
tctcccccat ngncggaang tgcacctgan accgggaacg gg                     282


<210> 102
<211> 290
<212> DNA
<213> Zea mays

<400> 102
ggacgcggca ccatgcgcgc cgagctggcc agtggcgacg tggccgtgtg ccccgagggc  60
accacgtgcc gggagccctt cctgctccgc ttctccaagc tcttcgcgga gctcagcgac  120
aggatcgtgc ccgtggcgat gaactaccgc gtggggctct tccacccgac gacggcgcgc  180
gggtggaaag ccatggaccc catcttcttc ttcatgaacn gcggcccgtg tacgaggtga  240
cgttcctgaa ccantccccg caaagcgacg tgcgcggcgg ggaagagccc               290


<210> 103
<211> 279
<212> DNA
<213> Zea mays

<400> 103
acgaggtgac gttcctgaac cagctccccg cagaggcgac gtgcgcggcg gggaagagcc  60
ccgttgatgt agccaactac gttcagcgga tactcgctgc cacgctcggg ttcgagtgca  120
ccaccctcac aaggaaggac aaatacacgg tgctcgccgg caacgacggc gtcctgaacg  180
ccaagccggc ggcggcccgg aagccggctt ggcagagccg cgtgaaggaa gtcctcgggt  240
tctgctccac taacaattac accttgccca gatctggac                         279


<210> 104
<211> 315
<212> DNA
<213> Zea mays

<400> 104
gcccgagcgc atcgtctact acacctacaa gctcatgggc atcaggctcg tcgtcaaggg  60
caccccgccg ccgccgccca agaagggcca cccgggcgtc ctcttcgtct gcaaccaccg  120
caccgtgctc gaccccgtcg aggtggccgt ggcgctgcgc cgcaangtca gctgcgtcac  180
```

```
tacagcatct ccaagttctc cgagctcatc tcgcccatca aggccgtagc agnaaagcag 240
gtcgcaaatg gagcagnagc gagtcgatgg aagngaattg gcgactggtc atctgcncga 300
aggnacactg cggag                                                  315
```

<210> 105
<211> 314
<212> DNA
<213> Zea mays

<400> 105
```
cgagacaccg agcacgtact accagcaaga tggtggcgtc tcccagattc aagcccatcg 60
aggagtgctg ctcggagggg cggtcggagc agacggtggc cgccgacctg acggcacgc 120
tgctcatctc caggagcgcg ttcccctact acctcctcgt ggctctcgag gccggcagcg 180
tcctccgcgc cgcgctgctg ctcctgtccg tgccgttcgt ctacgtcacc tacgccttct 240
tctccgagtc gctggccatc agcacgctgg tgtacatctc cgtggcgggg ctcaaggtgc 300
gcanatcgag atgg                                                   314
```

<210> 106
<211> 291
<212> DNA
<213> Zea mays

<400> 106
```
ctctgggtct ggggccgaga caccgagcac gtactaccag caagatggtg gcgtctccca 60
gattcaagcc catcgaggag tgctgctcgg aggggcggtc ggagcagacg gtggccgccg 120
acctggacgg cacgctgctc atntccagga gcgcgttccc ctactacctc ctcgtggctc 180
tcgaggccgg cagcgtcctc cgcgccgcgc tgctgctcct gtccgtgccg ttcgtctacg 240
tcacctacgc cttcttctcc gagtcgctgg ccatcagcac gctggtgtac a 291
```

<210> 107
<211> 300
<212> DNA
<213> Zea mays

<400> 107
```
gcacgcagca gtacgacgtc tctcctctgg gtctggggcc gagacaccga gcacgtacta 60
ccagcaagat ggtggcgtct cccagattca agcccatcga ggagtgctgc tcggaggggc 120
ggtcggagca gacggtggcc gccgacctgg acggcacgct gctcatctcc aggagcgcgt 180
tcccctacta cctcctcgtg gctctcgagg ccggcagcgt cctccgcgcc gcgctgctgc 240
tcctgtccgt gccgttcgtc tacgtcacct acgccttctt ctccgagtcg ctggccatca 300
```

<210> 108
<211> 284
<212> DNA
<213> Zea mays

<400> 108
```
gnggccgaga caccgagcac gtactaccag cangatggtg gcgtctccca gattcangcc 60
antcgaggag tgctgctcgg aggggcggtc ggagcagacg gtggccgccg acctggacgg 120
cacgctgctc atctccagga gcgcgttccc ctacnacctc ctcgtggctc tcgaggccgg 180
cagcgtcctc cgcgccgcgc tgctgctcct gtccgtgccg ttcgtctacg tcactacgcc 240
ttcttctccg agtcgctggc catcaanacg ctggtgtaca tctc 284
```

<210> 109
<211> 280
<212> DNA
<213> Zea mays

<400> 109
```
ctcctctggg tctggggccg agacaccgag cacgtactac cagcaagatg gtggcgtctc 60
ccagattcaa gcccatcgag gagtgctgct cggaggggcg gtcggagcag acggtggccg 120
ccgacctgga cggcacgctg ctcatctcca ggagcgcgtt ccnctactac ctcctcgtgg 180
ctctcgaggc cggcagcgtc ctccgcgccg cgctgctgct cctgtccgtn ccgttcgtct 240
acgtcaccta cgcnttnttc tccgagtcgc tggccatcag 280
```

<210> 110
<211> 287
<212> DNA
<213> Zea mays

```
<400> 110
cgtctctcct ctgggtctgg ggccgagaca ccgagcacgt actaccagca agatggtggc 60
gtctcccaga ttcaagccca tcgaggagtg ctgctcggag gggcggtcgg agcagacggt 120
ggccgccgac ctggacggca gctgctcatc tccaggagcg cgttccccta ctacctcctc 180
gtggctctcg aggccggcag cgtcctccgc ccgcgctgc tgctcctgtc cgtgccgttc 240
gtctacgtca ctacggcttc ttctccgagt cgctggccat cagcacg               287
```

```
<210> 111
<211> 286
<212> DNA
<213> Zea mays
```

```
<400> 111
cgcacagtta cgacgtctct cctctgggtc tggggccgag acaccgagca cgtactacca 60
gcaagatggt ggcgtctccc agattcaagc ccatcgagga gtgctgctcg gaggggcggt 120
cggagcagac ggtggccgcc gacctggacg gcacgctgct catctccagg agcgcgttcc 180
cctactactc ctcgtgctct cgaggccggc aggtcctccg cgccgcgctg tgctcctgtc 240
gtgcgttcgt ctagtcacta cgcttttctc gancgtggca ataana                286
```

```
<210> 112
<211> 323
<212> DNA
<213> Zea mays
```

```
<400> 112
gttattccct gaaggtacca caacaaatgg gagattcctg atttcgttcc aacatggtgc 60
attcatacct ggctaccctg ttcaacctgt tgttgtccgt tatccacatg tgcactttga 120
tcaatcatgg gggnatatat cgttattaaa gctcatgttt aagatgttca cccaatttca 180
taatttcatg gaggtagagt accttcctgt tgtctaccct cctgagatca agcaagagaa 240
tgcccttcat tttgcggagg ataccagcta tgctatggca cgtgccctca atgtcttgcc 300
aacttcctat tcatatggtg att                                         323
```

```
<210> 113
<211> 312
<212> DNA
<213> Zea mays
```

```
<400> 113
cgataaggcc cttttcgaag agcttctacc gtcggatcaa cagattcttg ccgagctgc 60
tgtggcttca gcttgtctgg gtggtggact ggtgggcagg tgttaaggta caactgcatg 120
cagatgagga aacttacaga tcaatgggta aagagcatgc actcatcata tcaaatcatc 180
ggagtgatat tgattggctc attggatgga tattggccca gcgttcaggg tgccttggaa 240
gtacacttgc tgtcatgaag aagtcatcca agttccttcc agttattggc tggtcaatgt 300
ggtttgcaga gt                                                     312
```

```
<210> 114
<211> 279
<212> DNA
<213> Zea mays
```

```
<400> 114
agtggggtct ccaaaggttg aaagacttcc ctagaccatt ttggctagct cttttgttg 60
agggtactcg ctttactcca gcaaagcttc tcgcagctca ggagtatgcg gcttcccagg 120
gcttaccagc tcctagaaat gtacttattc cacgtaccaa gggatttgta tctgccgtaa 180
gtattatgcg agattttgtt ccagccattt acgatacaac tgtaatagtt cctaaagatt 240
cccctcaacc aacaatgctg cggattttga aagggcaat                         279
```

```
<210> 115
<211> 304
<212> DNA
<213> Zea mays
```

```
<400> 115
cgtcaacgcc atccaggccg tcctatttgt gacgataagg cccttttcga agagcttcta 60
ccgtcggatc aacagattct tggccgagct gctgtggctt cagcttgtct gggtggtgga 120
ctggtgggca ggtgttaagg tacaactgca tgcagatgag gaaacttaca gatcaatggg 180
taaagagcat gcactcatca tatcaaatca tcggagtgat attgattggc tcatggatgg 240
atattggccc agcgttcagg gtgccttgga agtacattgc tgtcatgaag aagtcatcca 300
agtt                                                              304
```

```
<210> 116
<211> 259
<212> DNA
<213> Zea mays

<400> 116
cttcctcctg tccggcctca tcgtcaacgc catccaggcc gtcctatttg tgacgataag  60
gcccntttcg aagagcttct aacgtcggat caacagattc ntggccgagc tgctgtggct 120
tcagcttgtc tgggtggtgg acnggtgggc aggtgttaag gtacaactgc atgcngatga 180
ggaaacttac agatcnatgg gtanagagca tgcactcatc atatcaaatc atcggagtga 240
tattgattgg cncattgga                                              259

<210> 117
<211> 235
<212> DNA
<213> Zea mays

<400> 117
attccacgta ccaagggatt tgtatctgct gtaagtatta tgcgagattt tgttccagcc  60
atttatgata caactgtaat agttcctaaa gattcccctc aaccaacaat gctgcggatt 120
ttgaaagggc aatcatcagt gatacatgtc cgcatgaaac gtcatgcaat gagtgagatg 180
ccaaaatcag atgaggatgt ttcaaaatgg tgtaaagaca tttttgtggc aaagg       235

<210> 118
<211> 282
<212> DNA
<213> Zea mays

<400> 118
tgagatgcca aaatcagatg atgacgtttc aaaatggtgt aaagacattt ttgtgacaaa  60
ggatgcctta ctggacaaac atttggcaac aggcactttc gatgaggaga ttagacctat 120
cggccgccca gtgaaatcat tgctggtgac cctgttttgg tcgtgcctgc tgttgtttgg 180
tgccatcgag ttcttcaagt ggacgcagct cctatcgaca tggagaggag tggcattcac 240
tgccgcagga tggcgctcgt gacaggggtc atgcacgtct tc                    282

<210> 119
<211> 166
<212> DNA
<213> Zea mays

<400> 119
ctggtgggca ggcgttaagg tacaactaca tgcggatgag gacacttacc gatcaatggg  60
taaagagcat gcactcgtca tatcaaatca tcgaagtgat attgattggc ttattggatg 120
gatattggcc cagcgctcag ggtgccttgg aagtacgctc gctgtc               166

<210> 120
<211> 234
<212> DNA
<213> Zea mays

<400> 120
agtcanccaa gntccttcca gtcattggct ggtcaatgtg gtttgcagag tacctctttt  60
nggagaggag ctgggccaag gatgaaaaga cactaaagtg gggtctccaa aggttgaaag 120
acttccctag accatttngg ctagctcttn tttgtngagg gnantcgctt tactccagca 180
angnttntng aggnnncagn agnnncgggn ttcccanggg ttaacagncc cana        234

<210> 121
<211> 210
<212> DNA
<213> Zea mays

<400> 121
gtgagatgcn aaaatcagat gatgacgttt caaaatggtg taaagacatt tttgtggaca  60
aaggatgcct tactggacaa acatttggca acaggcactt tcgatgagga gattagacct 120
atcggccgcc cagtgaaatc atngctggtg accctgtnnt ggtcgtgcct gctgttgttt 180
ggtgccatcg agntcttcaa gtggacgcag                                  210

<210> 122
<211> 274
<212> DNA
```

<213> Zea mays

<400> 122
```
acncccgaat ccgccgcgcg cgcnccgtcc tcgtcgccgg cggaggcgcc cgcnaccgcc 60
cacagcagcc tatcgccgga gaaggaacgc cgcggggagc ttttccacng ccatctcccg 120
tctgacccct ccgagatcgn aagcggcggc catggcgatc ccgctcgtgc tcgtcgtgct 180
cccgctcggc ctcctcttcc tcctgtccgg cctcatcgtc aacaccatcc aggccatcct 240
atttgtgaca ataaggccct tttccaagag cttg.                             274
```

<210> 123
<211> 305
<212> DNA
<213> Zea mays

<400> 123
```
ttgcactgag gaaaggccat tagggatata tcaagtacat acataagagc agcttgatga 60
agttgcctat ttttagctgg gcatttcaca tttttgagtt tatcccggta gaacggaaat 120
gggagattga tgaagcaatt attcagaaca agctatcaaa atttaagaac ccgagagatc 180
ctatctggtt ggcggttttt cctgaaggca cggattatac tgagaagaaa tgcatcatga 240
gtcaagagta tgcttcagaa catggcttgc ctatgctaga acatgtcctc cttccaaaga 300
caagg                                                              305
```

<210> 124
<211> 279
<212> DNA
<213> Zea mays

<400> 124
```
ccagattttc tggacaatgt gtatggcgtt gatccttctg aagtccacat ccacgtcaga 60
atggttcagc tccatcacat ccccacaaca gaagacaaga taacagaatg gatggncgag 120
aggtttaggc agaaggacca gctcctggca gatttcttca tgaaggggca tttcctgatg 180
aaaggaactg aaaggagatc tgtcgacgcc gagtgcctgg caaactttct taaccagtag 240
tatgcttgac ggccnatctg gtttgtacct aaactcttt                        279
```

<210> 125
<211> 219
<212> DNA
<213> Zea mays

<400> 125
```
agattttntg gacaatgtgt atggngttga tccttntgaa gtncacatcc acgtnagaat 60
ggttcagctc catcacatcc ccacaacagn agacaagata acagaangga tggtagagag 120
gtttaggcag aaggaccagc tcctggcaga tttcttcatg aaggggcact ttcctgatga 180
aggaactgaa ggagatctgt cgacgccgaa gtgcctggc                        219
```

<210> 126
<211> 293
<212> DNA
<213> Zea mays

<400> 126
```
taccatagat gctgtgtacg acatcacgat cgcntacaaa caccggcngc ngacatttct 60
ngacaacgtc tacngcgtgg ntccttcgga agtccacatc cacatcanca gcatccaggt 120
ctccgacata ncggcgtccg aaaaacgggg tggctggcng gntnngtgga gcggttcaag 180
gcntnganna acgagctngc tgttcggggc tttctaccgc ggctggggcc aatttcnccc 240
cgaacgaaag ggaaaaaggg gaaccgaagg ggggaacctg ttngaacggg ncc          293
```

<210> 127
<211> 6
<212> PRT
<213> conserved sequence

<400> 127
```
Val Xaa Asn His Xaa Ser
 1               5
```

<210> 128
<211> 6
<212> PRT

```
<213> conserved sequence

<400> 128
Val Thr Tyr Ser Xaa Ser
  1               5


<210> 129
<211> 7
<212> PRT
<213> conserved sequence

<400> 129
Val Xaa Leu Thr Arg Xaa Arg
  1               5


<210> 130
<211> 5
<212> PRT
<213> conserved sequence

<400> 130
Cys Pro Glu Gly Thr
  1               5


<210> 131
<211> 5
<212> PRT
<213> conserved sequence

<400> 131
Ile Val Pro Val Ala
  1               5


<210> 132
<211> 7
<212> PRT
<213> conserved sequence

<400> 132
Leu Xaa Xaa Gly Asp Leu Val
  1               5


<210> 133
<211> 6
<212> PRT
<213> conserved sequence

<400> 133
Phe Xaa Xaa Gly Ala Phe
  1               5


<210> 134
<211> 6
<212> PRT
<213> Synthetic Oligonucleotide

<400> 134
Val Ala Asn Xaa Xaa Gln
  1               5


<210> 135
<211> 30
<212> DNA
```

<213> Synthetic Oligonucleotide

<400> 135
ccatccgctt caagggaacg acacccatca   30

<210> 136
<211> 31
<212> DNA
<213> Synthetic Oligonucleotide

<400> 136
tccctgtctt gcttgatgaa cttaaagctt g   31

<210> 137
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 137
acagcaggag tgtctgatga tggcagattc   30

<210> 138
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 138
actggagttc agccaaaaa tgcacctgtc   30

<210> 139
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 139
gatacaccct tgaaatcagg cgattttgct   30

<210> 140
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 140
ttgcaaattc aattcctgtt tcaccgggcc   30

<210> 141
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 141
gttttctgct attccagaag gcgtcaacaa   30

<210> 142
<211> 32
<212> DNA
<213> Synthetic Oligonucleotide

<400> 142
cattgaagat ccgtccgtga agttncctta cc   32

<210> 143
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 143
tcgagctgtg atcgatgatt ggctgtgaag   30

<210> 144

```
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 144
gtctcttcaa aaacacacac acacgtctct                                    30

<210> 145
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 145
gtctcttcaa aaacacacac acacgtctct                                    30

<210> 146
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 146
gtagagagcc ttacttgctt cggtttagtc                                    30

<210> 147
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 147
acgtcatcgt acctgttgct attgactcac                                    30

<210> 148
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 148
acttttccat tgtcagggac tcctcgacac                                    30

<210> 149
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 149
acggtgtagg aagggaaagg attcaaaagg                                    30

<210> 150
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 150
gcgatgaact acagagtcgg attcttcctc                                    30

<210> 151
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 151
ccggtttacg agattacgtt cttgaaccag                                    30

<210> 152
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 152
caatggagac aaggctcgaa agtgctaacc                                    30
```

```
<210> 153
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 153
attctctgaa catagttcgc cacggtcatg                                    30

<210> 154
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 154
gaaatccaac gccttcccaa tatcactctg                                    30

<210> 155
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 155
cttcaacttt ccatcaggat cttggcacgt                                    30

<210> 156
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 156
accacttgtt agagacctta cctgcttagg                                    30

<210> 157
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 157
tcctacctac accatccaat ttctcgaccc                                    30

<210> 158
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 158
ctgcgtcaag tgagcaactc agttcttgca                                    30

<210> 159
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 159
tgggaagcag cacgttgttc agtatcggaa                                    30

<210> 160
<211> 30
<212> DNA
<213> Synthetic Oligonucleotide

<400> 160
tagcctctgt gtaatctgtg ccctcgggga                                    30

<210> 161
<211> 1702
<212> DNA
<213> Simmondsia chinensis
```

<400> 161
gaattctagc ctctctcctc ctgcaattct acttgctttc tacgatcttt ccctctctct 60
ctctaaaacc ttaaaattgg aatggaatcg tttaaaaata tgatcttttt gtaattgaat 120
tagtataatt atatctgggt aatcttgaat ttgttggtga ggccatgggg atcccagctg 180
cggctgtgat tgtaccgctt ggcttgctct tcttcttctc tggtctcttc atcaacttca 240
ttcaggcaat ttgtttgtg ctcgtgcggc cactgtcaaa gnntacatac agaaggatta 300
acagggtgct ggtggaattg ttgtggcttg agctgatatg gctcgtagat tggtgggcaa 360
gtgttaagat caagttgttc acagatcctg ataccttcg gctaatgggt aaagagcatg 420
cacttgtgat atcaaaccac agaagtgata ttgattggct tgttggatgg gtgttggccc 480
agagatcagg ctgcctggga agcacactgg ctgtcatgaa gaaatcatca agtttctcc 540
cggtcatagg ttggtctatg tggtttctg agtacctttt tcttgagaga agctgggcca 600
aggatgaaag cacattgaag ttaggtcttc aacgcctcaa ggactaccct ctgcctttct 660
ggttggctct tttcgtagaa ggaacacgat ttacccaagc taaacttta gcagctcaag 720
aatatgctac ttcaatggga ttgccagttc ctagaaatac tttgatccct cgtactaagg 780
gatttgtttc agccgtgagc catatgcgtt cgtttgtccc ggccatatat gatgtaacgg 840
tggccatccc taaatcttct tcgcagccta caatgctcag acttttcaaa ggccagccat 900
ccacggttca tgtacacatc aagcgccgct cgatgaaaga tctccctgaa gcagcagatg 960
atgttgcaca atggtgtcga gacacattcg tcgcaaagga tgcactcctg acaagcata
1020
atgtagatga cactttcgga gatgagtatc tgcaggacac tggccggcct ttgaaatctc
1080
tctttgtagc agtctcttgg gcattgattc tcatcctggg aggtttgaaa ttcctacgat
1140
ggtcgtccct tctatcatca tggaaggggg tcgccttctc agccgcatgc cttgtgctcg
1200
tcaccattct tatgcagatc ttaatccaat tttctcaatc cgagcgctcg actcctgcta
1260
aggtagcccc aggaaagccc aagaacatgg tatcagaacc cacggaaacg caacgacata
1320
agcagcacta aaagtatata tggaccccaa ctaagaagat tcagacgcaa gccacagttg
1380
attcaactgt tcagaatgtc aaatatagtt tgagaaacaa aagatcaaga ttagctgatg
1440
aagagcctaa tgaacctaca tacttggatc tgtcgtcgcc accgtctgct gctagctcgt
1500
tatcagaatt cgtgattccg ggaccgatcc cggatcttag ccttctatgc atggattatg
1560
atagtatctt aaatttcttt aatgatgtac cggaattata atgttagtta attaggggga
1620
tgagcattgt ttgggtttat atcgtggtaa atccttgtat tgtttataag atttgaagaa
1680
aattcgattc gagtgctctg aa
1702

<210> 162
<211> 387
<212> PRT
<213> Simmondsia chinensis

<400> 162
Met Gly Ile Pro Ala Ala Ala Val Ile Val Pro Leu Gly Leu Leu Phe
 1   5   10   15

Phe Phe Ser Gly Leu Phe Ile Asn Phe Ile Gln Ala Ile Cys Phe Val
                20   25   30

Leu Val Arg Pro Leu Ser Lys Thr Tyr Arg Arg Ile Asn Arg Val Leu
        35   40   45

Val Glu Leu Leu Trp Leu Glu Leu Ile Trp Leu Val Asp Trp Trp Ala
    50   55   60

Ser Val Lys Ile Lys Leu Phe Thr Asp Pro Asp Thr Phe Arg Leu Met
65   70   75   80

Gly Lys Glu His Ala Leu Val Ile Ser Asn His Arg Ser Asp Ile Asp
                85   90   95

Trp Leu Val Gly Trp Val Leu Ala Gln Arg Ser Gly Cys Leu Gly Ser
            100   105   110

```
Thr Leu Ala Val Met Lys Lys Ser Ser Lys Phe Leu Pro Val Ile Gly
        115             120             125

Trp Ser Met Trp Phe Ser Glu Tyr Leu Phe Leu Glu Arg Ser Trp Ala
    130             135             .   140

Lys Asp Glu Ser Thr Leu Lys Leu Gly Leu Gln Arg Leu Lys Asp Tyr
145             150             155             160

Pro Leu Pro Phe Trp Leu Ala Leu Phe Val Glu Gly Thr Arg Phe Thr
            165             170             175

Gln Ala Lys Leu Leu Ala Ala Gln Glu Tyr Ala Thr Ser Met Gly Leu
        180             185             190     .

Pro Val Pro Arg Asn Thr Leu Ile Pro Arg Thr Lys Gly Phe Val Ser
        195             200             205

Ala Val Ser His Met Arg Ser Phe Val Pro Ala Ile Tyr Asp Val Thr
    210             215             220

Val Ala Ile Pro Lys Ser Ser Ser Gln Pro Thr Met Leu Arg Leu Phe
225             230             235             240

Lys Gly Gln Pro Ser Thr Val His Val His Ile Lys Arg Arg Ser Met
            245             250             255

Lys Asp Leu Pro Glu Ala Ala Asp Asp Val Ala Gln Trp Cys Arg Asp
            260             265             270

Thr Phe Val Ala Lys Asp Ala Leu Leu Asp Lys His Asn Val Asp Asp
        275             280             285

Thr Phe Gly Asp Glu Tyr Leu Gln Asp Thr Gly Arg Pro Leu Lys Ser
        290             295             300

Leu Phe Val Ala Val Ser Trp Ala Leu Ile Leu Ile Leu Gly Gly Leu
305             310             315             320

Lys Phe Leu Arg Trp Ser Ser Leu Leu Ser Ser Trp Lys Gly Val Ala
            325             330             335

Phe Ser Ala Ala Cys Leu Val Leu Val Thr Ile Leu Met Gln Ile Leu
            340             345             350

Ile Gln Phe Ser Gln Ser Glu Arg Ser Thr Pro Ala Lys Val Ala Pro
        355             360             365

Gly Lys Pro Lys Asn Met Val Ser Glu Pro Thr Glu Thr Gln Arg His
370             375             380

Lys Gln His
385
```

```
<210> 163
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 163
aagcttgcat gcgtcgacac aatggttcat gcgaccaagt cag        43

<210> 164
<211> 35
```

```
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 164
ggtaccgtcg actcacttct tggtgttgtt gatag                          35

<210> 165
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 165
ggatccgcgg ccgcacaatg acgagcttta ctacttccct tcat                44

<210> 166
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 166
ggatcccctg caggttagag atccattgat tctgcaat                       38

<210> 167
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 167
ggatccgcgg ccgcataatg gaatcagagc tcaaagat                       38

<210> 168
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 168
ggatcccctg caggtcattc ttctttctga tggaaatc                       38

<210> 169
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 169
ggatccgcgg ccgcacaatg actcgttcac aagatgtttc a                   41
```

```
<210> 170
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 170
ggatcccctg caggtcactt ctcttccaat ctagccag                          38

<210> 171
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 171
ggatccgcgg ccgcacaatg tccggtaata agatctcgac tcttca                 46

<210> 172
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 172
ggatcccctg caggttattt tttcttgaca actccgttat taccgg                 46

<210> 173
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 173
atatccgcgg ccgcacaatg gttatggagc aagctggaa                         39

<210> 174
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 174
ggatcccctg caggtcaatg gagacaaggc tcgaaagt                          38

<210> 175
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 175
```

```
ggatccgcgg ccgcacaatg tccgccaaga tttcaatatt cc                    42
```

<210> 176
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 176
```
ggatcccctg caggttaatt tttcttaact actccatt                         38
```

<210> 177
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 177
```
ggatccgcgg ccgcacaatg ggagctcagg agaaacggcg cc                    42
```

<210> 178
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 178
```
ggatcccctg caggtcacgt cttctccttc ttcaccgg                         38
```

<210> 179
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 179
```
ggatccgcgg ccgcacaatg gcggatcctg atctgtcttc tcct                  44
```

<210> 180
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 180
```
ggatcccctg caggttatgt tggggccaag tcaggtgcaa agat                  44
```

<210> 181
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 181
ggatccgcgg ccgcaaaatg gaaaaaaaga gtgtaccaaa ttct   44

<210> 182
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 182
ggatcccctg caggttattt gtttactaat ttgagggaat tttttg   46

<210> 183
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 183
tcgacctgca ggaagcttaa ggatggtgat tgctgc   36

<210> 184
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 184
ggatccgcgg ccgcttactt ctccttctcc g   31

<210> 185
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 185
ggatccgcgg ccgcacaatg tcttttaggg atgtcctag   39

<210> 186
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 186
ggatcccctg caggtcaatc atccttaccc tttggtttac c   41

<210> 187
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 187
atgtctttta gggatgtcct agaaagagga gatgaatttt ctgtgcggta tttcacaccg 60

<210> 188
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 188
tcaatcatcc ttaccctttg gtttaccctc tggaggcaga agattgtact gagagtgcac 60

<210> 189
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 189
ggatccgcgg ccgcacaatg aagcattccc aaaaataccg tagg   44

<210> 190
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 190
ggatcccctg caggtcaatg atttttttc atcacaaata c   41

<210> 191
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 191
atgaagcatt cccaaaaata ccgtaggtat ggaatttatg ctgtgcggta tttcacaccg 60

<210> 192
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 192
tcaatgattt ttttcatca caaatacaag aataagaaaa agattgtact gagagtgcac 60

<210> 193
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 193
ggatccgcgg ccgcacaatg ggttttgttg atttcttcga aac   43

<210> 194
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 194
ggatcccctg caggttattt ggtctcaatt ttaatatttt tttgc   45

<210> 195
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 195
atgggttttg ttgatttctt cgaaacatat atggtcggtt ctgtgcggta tttcacaccg 60

<210> 196
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 196
ttatttggtc tcaattttaa tatttttttg caaggactcg agattgtact gagagtgcac 60

<210> 197
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 197
ggatccgcgg ccgcacaatg gaaaagtaca ccaattggag agac   44

<210> 198
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 198
ggatcccctg caggctactt cctcttttta cgttgatcgc tg   42

<210> 199
<211> 60

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 199
atggaaaagt acaccaattg gagagacaat ggtacgggaa ctgtgcggta tttcacaccg 60

<210> 200
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 200
ctacttcctc tttttacgtt gatcgctgat atattccttc agattgtact gagagtgcac 60

<210> 201
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 201
ggatccgcgg ccgcacaatg cctgcaccaa aactcacgga g                      41

<210> 202
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 202
ggatcccctg caggctacgc atctccttct ttcccttc                         38

<210> 203
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 203
atgcctgcac caaaactcac ggagaaatct gcctcttcca ctgtgcggta tttcacaccg 60

<210> 204
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 204
ctacgcatct ccttctttcc cttcttcttc ttcttcctct agattgtact gagagtgcac 60
```

```
<210> 205
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 205
ggatccgcgg ccgcacaatg tctgctcccg ctgccgatca taacgc          46

<210> 206
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 206
ggatcccctg caggtcattc tttcttttcg tgttctcttt tctg            44

<210> 207
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 207
atgtctgctc ccgctgccga tcataacgct gccaaaccta ctgtgcggta tttcacaccg 60

<210> 208
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 208
tcattctttc ttttcgtgtt ctcttttctg tcttaccagc agattgtact gagagtgcac 60

<210> 209
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 209
ggatccgcgg ccgcacaatg ctgcatcaaa aaatagctca taaagttcg            49

<210> 210
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 210
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ggatcccctg caggtcaaaa aataaaacaa taaagtttat aaactaacc   49

<210> 211
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 211
atgctgcatc aaaaaatagc tcataaagtt cgaaaagtcg ctgtgcggta tttcacaccg 60

<210> 212
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 212
tcaaaaaata aaacaataaa gtttataaac taaccaaatt agattgtact gagagtgcac 60

<210> 213
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 213
ggatccgcgg ccgcacaatg agtgtgatag gtaggttctt g   41

<210> 214
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 214
ggatcccctg caggttaatg catctttttt acagatgaac c   41

<210> 215
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 215
atgagtgtga taggtaggtt cttgtattac ttgaggtccg ctgtgcggta tttcacaccg 60

<210> 216
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 216
ttaatgcatc tttttttacag atgaaccttc gttatgggta agattgtact gagagtgcac 60

<210> 217
<211> 381
<212> PRT
<213> Saccharomyces sp.

<220>

<400> 217

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Met Ser Phe Arg Asp Val Leu Glu Arg Gly Asp Glu Phe Leu Glu Ala
1               5                   10                  15

Tyr Pro Arg Arg Ser Pro Leu Trp Arg Phe Leu Ser Tyr Ser Thr Ser
                20              25                  30

Leu Leu Thr Phe Gly Val Ser Lys Leu Leu Leu Phe Thr Cys Tyr Asn
        35                  40                  45

Val Lys Leu Asn Gly Phe Glu Lys Leu Glu Thr Ala Leu Glu Arg Ser
    50                  55                  60

Lys Arg Glu Asn Arg Gly Leu Met Thr Val Met Asn His Met Ser Met
65                  70                  75                  80

Val Asp Asp Pro Leu Val Trp Ala Thr Leu Pro Tyr Lys Leu Phe Thr
                85                  90                  95

Ser Leu Asp Asn Ile Arg Trp Ser Leu Gly Ala His Asn Ile Cys Phe
            100                 105                 110

Gln Asn Lys Phe Leu Ala Asn Phe Phe Ser Leu Gly Gln Val Leu Ser
            115                 120                 125

Thr Glu Arg Phe Gly Val Gly Pro Phe Gln Gly Ser Ile Asp Ala Ser
    130                 135                 140

Ile Arg Leu Leu Ser Pro Asp Asp Thr Leu Asp Leu Glu Trp Thr Pro
145                 150                 155                 160

His Ser Glu Val Ser Ser Ser Leu Lys Lys Ala Tyr Ser Pro Pro Ile
                165                 170                 175

Ile Arg Ser Lys Pro Ser Trp Val His Val Tyr Pro Glu Gly Phe Val
            180                 185                 190

Leu Gln Leu Tyr Pro Pro Phe Glu Asn Ser Met Arg Tyr Phe Lys Trp
            195                 200                 205

Gly Ile Thr Arg Met Ile Leu Glu Ala Thr Lys Pro Pro Ile Val Val
    210                 215                 220

Pro Ile Phe Ala Thr Gly Phe Glu Lys Ile Ala Ser Glu Ala Val Thr
225                 230                 235                 240

Asp Ser Met Phe Arg Gln Ile Leu Pro Arg Asn Phe Gly Ser Glu Ile
                245                 250                 255

Asn Val Thr Ile Gly Asp Pro Leu Asn Asp Asp Leu Ile Asp Arg Tyr
            260                 265                 270

Arg Lys Glu Trp Thr His Leu Val Glu Lys Tyr Tyr Asp Pro Lys Asn
    275                 280                 285

Pro Asn Asp Leu Ser Asp Glu Leu Lys Tyr Gly Lys Glu Ala Gln Asp
    290                 295                 300

Leu Arg Ser Arg Leu Ala Ala Glu Leu Arg Ala His Val Ala Glu Ile
```

```
  305                       310                      315                       320
  Arg Asn Glu Val Arg Lys Leu Pro Arg Glu Asp Pro Arg Phe Lys Ser
                  325                  330                  335
  Pro Ser Trp Trp Lys Arg Phe Asn Thr Thr Glu Gly Lys Ser Asp Pro
                  340                  345                  350
  Asp Val Lys Val Ile Gly Glu Asn Trp Ala Ile Arg Arg Met Gln Lys
                  355                  360                  365
  Phe Leu Pro Pro Glu Gly Lys Pro Lys Gly Lys Asp Asp
      370                  375                  380
```

```
<210> 218
<211> 396
<212> PRT
<213> Saccharomyces sp.

<220>

<400> 218
Met Lys His Ser Gln Lys Tyr Arg Arg Tyr Gly Ile Tyr Glu Lys Thr
  1               5                   10                  15
Gly Asn Pro Phe Ile Lys Gly Leu Gln Arg Leu Leu Ile Ala Cys Leu
                20                  25                  30
Phe Ile Ser Gly Ser Leu Ser Ile Val Val Phe Gln Ile Cys Leu Gln
            35                  40                  45
Val Leu Leu Pro Trp Ser Lys Ile Arg Phe Gln Asn Gly Ile Asn Gln
        50                  55                  60
Ser Lys Lys Ala Phe Ile Val Leu Leu Cys Met Ile Leu Asn Met Val
65                  70                  75                  80
Ala Pro Ser Ser Leu Asn Val Thr Phe Glu Thr Ser Arg Pro Leu Lys
                85                  90                  95
Asn Ser Ser Asn Ala Lys Pro Cys Phe Arg Phe Lys Asp Arg Ala Ile
            100                 105                 110
Ile Ile Ala Asn His Gln Met Tyr Ala Asp Trp Ile Tyr Leu Trp Trp
        115                 120                 125
Leu Ser Phe Val Ser Asn Leu Gly Gly Asn Val Tyr Ile Ile Leu Lys
    130                 135                 140
Lys Ala Leu Gln Tyr Ile Pro Leu Leu Gly Phe Gly Met Arg Asn Phe
145                 150                 155                 160
Lys Phe Ile Phe Leu Ser Arg Asn Trp Gln Lys Asp Glu Lys Ala Leu
                165                 170                 175
Thr Asn Ser Leu Val Ser Met Asp Leu Asn Ala Arg Cys Lys Gly Pro
            180                 185                 190
Leu Thr Asn Tyr Lys Ser Cys Tyr Ser Lys Thr Asn Glu Ser Ile Ala
        195                 200                 205
Ala Tyr Asn Leu Ile Met Phe Pro Glu Gly Thr Asn Leu Ser Leu Lys
    210                 215                 220
Thr Arg Glu Lys Ser Glu Ala Phe Cys Gln Arg Ala His Leu Asp His
225                 230                 235                 240
Val Gln Leu Arg His Leu Leu Leu Pro His Ser Lys Gly Leu Lys Phe
                245                 250                 255
```

Ala Val Glu Lys Leu Ala Pro Ser Leu Asp Ala Ile Tyr Asp Val Thr
            260   265   270

Ile Gly Tyr Ser Pro Ala Leu Arg Thr Glu Tyr Val Gly Thr Lys Phe
        275   280   285

Thr Leu Lys Lys Ile Phe Leu Met Gly Val Tyr Pro Glu Lys Val Asp
    290   295   300

Phe Tyr Ile Arg Glu Phe Arg Val Asn Glu Ile Pro Leu Gln Asp Asp
305   310   315   320

Glu Val Phe Phe Asn Trp Leu Leu Gly Val Trp Lys Glu Lys Asp Gln
            325   330   335

Leu Leu Glu Asp Tyr Tyr Asn Thr Gly Gln Phe Lys Ser Asn Ala Lys
            340   345   350

Asn Asp Asn Gln Ser Ile Val Val Thr Thr Gln Thr Thr Gly Phe Gln
            355   360   365

His Glu Thr Leu Thr Pro Arg Ile Leu Ser Tyr Tyr Gly Phe Phe Ala
    370   375   380

Phe Leu Ile Leu Val Phe Val Met Lys Lys Asn His
385   390   395

<210> 219
<211> 479
<212> PRT
<213> Saccharomyces sp.

<220>

<400> 219
Met Gly Phe Val Asp Phe Phe Glu Thr Tyr Met Val Gly Ser Arg Val
  1   5   10   15

Gln Phe Lys Gln Leu Asp Ile Ser Asp Trp Leu Ser Leu Thr Pro Arg
            20   25   30

Leu Leu Ile Leu Phe Gly Tyr Phe Tyr Leu His Ser Phe Phe Thr Ala
        35   40   45

Ile Asn Gln Phe Leu Gln Phe Ile Asn Thr Asn Ser Phe Cys Leu Arg
    50   55   60

Leu His Leu Leu Tyr Asp Arg Phe Trp Ser His Val Pro Ile Ile Gly
65   70   75   80

Glu Tyr Lys Ile Arg Leu Leu Ser Arg Ala Leu Thr Tyr Ser Lys Leu
            85   90   95

Lys Ile Ile Pro Thr Leu Asp Lys Val Leu Glu Ala Ile Glu Ile Trp
            100   105   110

Phe Gln Leu His Leu Val Glu Met Thr Phe Glu Lys Lys Lys Asn Val
            115   120   125

Gln Ile Phe Ile Thr Glu Gly Ser Asp Asp Leu Asn Phe Phe Lys Asp
    130   135   140

Ser Lys Phe Gln Thr Thr Leu Met Ile Cys Asn His Arg Ser Val Asn
145   150   155   160

Asp Tyr Thr Leu Ile Asn Tyr Leu Phe Leu Lys Ser Cys Pro Thr Lys
            165   170   175

```
Phe Tyr Thr Lys Trp Glu Phe Leu Gln Lys Leu Arg Lys Gly Glu Asp
            180                 185                 190

Leu Ala Glu Trp Pro Gln Leu Lys Phe Leu Gly Trp Gly Lys Met Phe
        195                 200                 205

Asn Phe Pro Arg Leu Asp Leu Leu Lys Asn Ile Phe Phe Lys Asp Glu
    210                 215                 220

Thr Leu Ala Leu Ser Ser Asn Glu Leu Arg Asp Ile Leu Glu Arg Gln
225                 230                 235                 240

Asn Asn Gln Ala Ile Thr Ile Phe Pro Glu Val Asn Ile Met Ser Leu
                245                 250                 255

Glu Leu Ser Ile Ile Gln Arg Lys Leu His Gln Asp Phe Pro Phe Val
            260                 265                 270

Ile Asn Phe Tyr Asn Leu Leu Tyr Pro Arg Phe Lys Asn Phe Thr Thr
        275                 280                 285

Leu Met Ala Ala Phe Ser Ser Ile Lys Asn Ile Lys Arg Lys Lys Asn
    290                 295                 300

Arg Asn Asn Ile Ile Lys Glu Ala Arg Tyr Leu Phe His Arg Glu Leu
305                 310                 315                 320

Asp Lys Leu Val His Lys Ser Met Lys Met Glu Ser Ser Lys Val Ser
                325                 330                 335

Asp Lys Thr Thr Pro Pro Met Ile Val Asp Asn Ser Tyr Leu Leu Thr
            340                 345                 350

Lys Lys Glu Glu Ile Ser Ser Gly Lys Pro Lys Val Val Arg Ile Asn
        355                 360                 365

Pro Tyr Ile Tyr Asp Val Thr Ile Ile Tyr Tyr Arg Val Lys Tyr Thr
    370                 375                 380

Asp Ser Gly His Asp His Thr Asn Gly Asp Leu Arg Leu His Lys Gly
385                 390                 395                 400

Tyr Gln Leu Glu Gln Ile Ser Pro Thr Ile Phe Glu Met Ile Gln Pro
                405                 410                 415

Glu Met Glu Ser Glu Asn Asn Ile Lys Asp Lys Asp Pro Ile Val Val
            420                 425                 430

Met Val Asn Val Lys Lys His Gln Ile Gln Pro Leu Leu Ala Tyr Asn
        435                 440                 445

Asp Glu Ser Leu Glu Lys Trp Leu Glu Asn Arg Trp Ile Glu Lys Asp
    450                 455                 460

Arg Leu Ile Glu Ser Leu Gln Lys Asn Ile Lys Ile Glu Thr Lys
465                 470                 475
```

```
<210> 220
<211> 300
<212> PRT
<213> Saccharomyces sp.

<400> 220
Met Glu Lys Tyr Thr Asn Trp Arg Asp Asn Gly Thr Gly Ile Ala Pro
  1           5              10                 15

Phe Leu Pro Asn Thr Ile Arg Lys Pro Ser Lys Val Met Thr Ala Cys
        20                 25                 30
```

```
Leu Leu Gly Ile Leu Gly Val Lys Thr Ile Ile Met Leu Pro Leu Ile
        35                  40                  45
Met Leu Tyr Leu Leu Thr Gly Gln Asn Asn Leu Leu Gly Leu Ile Leu
    50                  55                  60
Lys Phe Thr Phe Ser Trp Lys Glu Glu Ile Thr Val Gln Gly Ile Lys
65                  70                  75                      80
Lys Arg Asp Val Arg Lys Ser Lys His Tyr Pro Gln Lys Gly Lys Leu
                85                  90                  95
Tyr Ile Cys Asn Cys Thr Ser Pro Leu Asp Ala Phe Ser Val Val Leu
            100                 105                 110
Leu Ala Gln Gly Pro Val Thr Leu Leu Val Pro Ser Asn Asp Ile Val
        115                 120                 125
Tyr Lys Val Ser Ile Arg Glu Phe Ile Asn Phe Ile Leu Ala Gly Gly
    130                 135                 140
Leu Asp Ile Lys Leu Tyr Gly His Glu Val Ala Glu Leu Ser Gln Leu
145                 150                 155                 160
Gly Asn Thr Val Asn Phe Met Phe Ala Glu Gly Thr Ser Cys Asn Gly
                165                 170                 175
Lys Ser Val Leu Pro Phe Ser Ile Thr Gly Lys Lys Leu Lys Glu Phe
            180                 185                 190
Ile Asp Pro Ser Ile Thr Thr Met Asn Pro Ala Met Ala Lys Thr Lys
        195                 200                 205
Lys Phe Glu Leu Gln Thr Ile Gln Ile Lys Thr Asn Lys Thr Ala Ile
    210                 215                 220
Thr Thr Leu Pro Ile Ser Asn Met Glu Tyr Leu Ser Arg Phe Leu Asn
225                 230                 235                 240
Lys Gly Ile Asn Val Lys Cys Lys Ile Asn Glu Pro Gln Val Leu Ser
                245                 250                 255
Asp Asn Leu Glu Glu Leu Arg Val Ala Leu Asn Gly Gly Asp Lys Tyr
            260                 265                 270
Lys Leu Val Ser Arg Lys Leu Asp Val Glu Ser Lys Arg Asn Phe Val
        275                 280                 285
Lys Glu Tyr Ile Ser Asp Gln Arg Lys Lys Arg Lys
    290                 295                 300


<210> 221
<211> 759
<212> PRT
<213> Saccharomyces sp.

<400> 221
Met Pro Ala Pro Lys Leu Thr Glu Lys Phe Ala Ser Ser Lys Ser Thr
    1               5                   10                  15
Gln Lys Thr Thr Asn Tyr Ser Ser Ile Glu Ala Lys Ser Val Lys Thr
                20                  25                  30
Ser Ala Asp Gln Ala Tyr Ile Tyr Gln Glu Pro Ser Ala Thr Lys Lys
        35                  40                  45
Ile Leu Tyr Ser Ile Ala Thr Trp Leu Leu Tyr Asn Ile Phe His Cys
    50                  55                  60
```

```
Phe Phe Arg Glu Ile Arg Gly Arg Gly Ser Phe Lys Val Pro Gln Gln
65              70                75                    80

Gly Pro Val Ile Phe Val Ala Ala Pro His Ala Asn Gln Phe Val Asp
                85                90                    95

Pro Val Ile Leu Met Gly Glu Val Lys Lys Ser Val Asn Arg Arg Val
            100                105                110

Ser Phe Leu Ile Ala Glu Ser Ser Leu Lys Gln Pro Pro Ile Gly Phe
        115                120                125

Leu Ala Ser Phe Phe Met Ala Ile Gly Val Val Arg Pro Gln Asp Asn
    130                135                140

Leu Lys Pro Ala Glu Gly Thr Ile Arg Val Asp Pro Thr Asp Tyr Lys
145                150                155                160

Arg Val Ile Gly His Asp Thr His Phe Leu Thr Asp Cys Met Pro Lys
            165                170                175

Gly Leu Ile Gly Leu Pro Lys Ser Met Gly Phe Gly Glu Ile Gln Ser
            180                185                190

Ile Glu Ser Asp Thr Ser Leu Thr Leu Arg Lys Glu Phe Lys Met Ala
        195                200                205

Lys Pro Glu Ile Lys Thr Ala Leu Leu Thr Gly Thr Thr Tyr Lys Tyr
    210                215                220

Ala Ala Lys Val Asp Gln Ser Cys Val Tyr His Arg Val Phe Glu His
225                230                235                240

Leu Ala His Asn Asn Cys Ile Gly Ile Phe Pro Glu Gly Gly Ser His
            245                250                255

Asp Arg Thr Asn Leu Leu Pro Leu Lys Ala Gly Val Ala Ile Met Ala
            260                265                270

Leu Gly Cys Met Asp Lys His Pro Asp Val Asn Val Lys Ile Val Pro
        275                280                285

Cys Gly Met Asn Tyr Phe His Pro His Lys Phe Arg Ser Arg Ala Val
    290                295                300

Val Glu Phe Gly Asp Pro Ile Glu Ile Pro Lys Glu Leu Val Ala Lys
305                310                315                320

Tyr His Asn Pro Glu Thr Asn Arg Asp Ala Val Lys Glu Leu Leu Asp
            325                330                335

Thr Ile Ser Lys Gly Leu Gln Ser Val Thr Val Thr Cys Ser Asp Tyr
            340                345                350

Glu Thr Leu Met Val Val Gln Thr Ile Arg Arg Leu Tyr Met Thr Gln
        355                360                365

Phe Ser Thr Lys Leu Pro Leu Pro Leu Ile Val Glu Met Asn Arg Arg
    370                375                380

Met Val Lys Gly Tyr Glu Phe Tyr Arg Asn Asp Pro Lys Ile Ala Asp
385                390                395                400

Leu Thr Lys Asp Ile Met Ala Tyr Asn Ala Ala Leu Arg His Tyr Asn
            405                410                415

Leu Pro Asp His Leu Val Glu Glu Ala Lys Val Asn Phe Ala Lys Asn
            420                425                430
```

```
Leu Gly Leu Val Phe Phe Arg Ser Ile Gly Leu Cys Ile Leu Phe Ser
        435                     440                 445

Leu Ala Met Pro Gly Ile Ile Met Phe Ser Pro Val Phe Ile Leu Ala
        450             455                 460

Lys Arg Ile Ser Gln Glu Lys Ala Arg Thr Ala Leu Ser Lys Ser Thr
465                 470                 475                     480

Val Lys Ile Lys Ala Asn Asp Val Ile Ala Thr Trp Lys Ile Leu Ile
                485                 490                 495

Gly Met Gly Phe Ala Pro Leu Leu Tyr Ile Phe Trp Ser Val Leu Ile
            500                 505                 510

Thr Tyr Tyr Leu Arg His Lys Pro Trp Asn Lys Ile Tyr Val Phe Ser
        515                 520                 525

Gly Ser Tyr Ile Ser Cys Val Ile Val Thr Tyr Ser Ala Leu Ile Val
        530             535                 540

Gly Asp Ile Gly Met Asp Gly Phe Lys Ser Leu Arg Pro Leu Val Leu
545                 550                 555                 560

Ser Leu Thr Ser Pro Lys Gly Leu Gln Lys Leu Gln Lys Asp Arg Arg
                565                 570                 575

Asn Leu Ala Glu Arg Ile Ile Glu Val Val Asn Asn Phe Gly Ser Glu
            580                 585                 590

Leu Phe Pro Asp Phe Asp Ser Ala Ala Leu Arg Glu Glu Phe Asp Val
        595                 600                 605

Ile Asp Glu Glu Glu Glu Asp Arg Lys Thr Ser Glu Leu Asn Arg Arg
        610                 615                 620

Lys Met Leu Arg Lys Gln Lys Ile Lys Arg Gln Glu Lys Asp Ser Ser
625                 630                 635                 640

Ser Pro Ile Ile Ser Gln Arg Asp Asn His Asp Ala Tyr Glu His His
                645                 650                 655

Asn Gln Asp Ser Asp Gly Val Ser Leu Val Asn Ser Asp Asn Ser Leu
            660                 665                 670

Ser Asn Ile Pro Leu Phe Ser Ser Thr Phe His Arg Lys Ser Glu Ser
            675                 680                 685

Ser Leu Ala Ser Thr Ser Val Ala Pro Ser Ser Ser Ser Glu Phe Glu
        690                 695                 700

Val Glu Asn Glu Ile Leu Glu Glu Lys Asn Gly Leu Ala Ser Lys Ile
705                 710                 715                 720

Ala Gln Ala Val Leu Asn Lys Arg Ile Gly Glu Asn Thr Ala Arg Glu
                725                 730                 735

Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
            740                 745                 750

Glu Gly Lys Glu Gly Asp Ala
            755
```

<210> 222
<211> 743
<212> PRT
<213> Saccharomyces sp.

<400> 222

```
Met Ser Ala Pro Ala Ala Asp His Asn Ala Ala Lys Pro Ile Pro His
 1               5               10              15

Val Pro Gln Ala Ser Arg Arg Tyr Lys Asn Ser Tyr Asn Gly Phe Val
            20              25              30

Tyr Asn Ile His Thr Trp Leu Tyr Asp Val Ser Val Phe Leu Phe Asn
        35              40              45

Ile Leu Phe Thr Ile Phe Phe Arg Glu Ile Lys Val Arg Gly Ala Tyr
    50              55              60

Asn Val Pro Glu Val Gly Val Pro Thr Ile Leu Val Cys Ala Pro His
65              70              75              80

Ala Asn Gln Phe Ile Asp Pro Ala Leu Val Met Ser Gln Thr Arg Leu
            85              90              95

Leu Lys Thr Ser Ala Gly Lys Ser Arg Ser Arg Met Pro Cys Phe Val
        100             105             110

Thr Ala Glu Ser Ser Phe Lys Lys Arg Phe Ile Ser Phe Phe Gly His
    115             120             125

Ala Met Gly Gly Ile Pro Val Pro Arg Ile Gln Asp Asn Leu Lys Pro
    130             135             140

Val Asp Glu Asn Leu Glu Ile Tyr Ala Pro Asp Leu Lys Asn His Pro
145             150             155             160

Glu Ile Ile Lys Gly Arg Ser Lys Asn Pro Gln Thr Thr Pro Val Asn
            165             170             175

Phe Thr Lys Arg Phe Ser Ala Lys Ser Leu Leu Gly Leu Pro Asp Tyr
        180             185             190

Leu Ser Asn Ala Gln Ile Lys Glu Ile Pro Asp Asp Glu Thr Ile Ile
    195             200             205

Leu Ser Ser Pro Phe Arg Thr Ser Lys Ser Lys Val Val Glu Leu Leu
    210             215             220

Thr Asn Gly Thr Asn Phe Lys Tyr Ala Glu Lys Ile Asp Asn Thr Glu
225             230             235             240

Thr Phe Gln Ser Val Phe Asp His Leu His Thr Lys Gly Cys Val Gly
            245             250             255

Ile Phe Pro Glu Gly Gly Ser His Asp Arg Pro Ser Leu Leu Pro Ile
            260             265             270

Lys Ala Gly Val Ala Ile Met Ala Leu Gly Ala Val Ala Ala Asp Pro
        275             280             285

Thr Met Lys Val Ala Val Val Pro Cys Gly Leu His Tyr Phe His Arg
    290             295             300

Asn Lys Phe Arg Ser Arg Ala Val Leu Glu Tyr Gly Glu Pro Ile Val
305             310             315             320

Val Asp Gly Lys Tyr Gly Glu Met Tyr Lys Asp Ser Pro Arg Glu Thr
            325             330             335

Val Ser Lys Leu Leu Lys Lys Ile Thr Asn Ser Leu Phe Ser Val Thr
        340             345             350

Glu Asn Ala Pro Asp Tyr Asp Thr Leu Met Val Ile Gln Ala Ala Arg
    355             360             365

Arg Leu Tyr Gln Pro Val Lys Val Arg Leu Pro Leu Pro Ala Ile Val
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        370                     375                     380
Glu Ile Asn Arg Arg Leu Leu Phe Gly Tyr Ser Lys Phe Lys Asp Asp
385                 390                 395                 400

Pro Arg Ile Ile His Leu Lys Lys Leu Val Tyr Asp Tyr Asn Arg Lys
                405                 410                 415

Leu Asp Ser Val Gly Leu Lys Asp His Gln Val Met Gln Leu Lys Thr
            420                 425                 430

Thr Lys Leu Glu Ala Leu Arg Cys Phe Val Thr Leu Ile Val Arg Leu
        435                 440                 445

Ile Lys Phe Ser Val Phe Ala Ile Leu Ser Leu Pro Gly Ser Ile Leu
    450                 455                 460

Phe Thr Pro Ile Phe Ile Ile Cys Arg Val Tyr Ser Glu Lys Lys Ala
465                 470                 475                 480

Lys Glu Gly Leu Lys Lys Ser Leu Val Lys Ile Lys Gly Thr Asp Leu
            485                 490                 495

Leu Ala Thr Trp Lys Leu Ile Val Ala Leu Ile Leu Ala Pro Ile Leu
            500                 505                 510

Tyr Val Thr Tyr Ser Ile Leu Leu Ile Ile Leu Ala Arg Lys Gln His
        515                 520                 525

Tyr Cys Arg Ile Trp Val Pro Ser Asn Asn Ala Phe Ile Gln Phe Val
    530                 535                 540

Tyr Phe Tyr Ala Leu Leu Val Phe Thr Thr Tyr Ser Ser Leu Lys Thr
545                 550                 555                 560

Gly Glu Ile Gly Val Asp Leu Phe Lys Ser Leu Arg Pro Leu Phe Val
                565                 570                 575

Ser Ile Val Tyr Pro Gly Lys Lys Ile Glu Glu Ile Gln Thr Thr Arg
            580                 585                 590

Lys Asn Leu Ser Leu Glu Leu Thr Ala Val Cys Asn Asp Leu Gly Pro
        595                 600                 605

Leu Val Phe Pro Asp Tyr Asp Lys Leu Ala Thr Glu Ile Phe Ser Lys
    610                 615                 620

Arg Asp Gly Tyr Asp Val Ser Ser Asp Ala Glu Ser Ser Ile Ser Arg
625                 630                 635                 640

Met Ser Val Gln Ser Arg Ser Arg Ser Ser Ile His Ser Ile Gly
            645                 650                 655

Ser Leu Ala Ser Asn Ala Leu Ser Arg Val Asn Ser Arg Gly Ser Leu
            660                 665                 670

Thr Asp Ile Pro Ile Phe Ser Asp Ala Lys Gln Gly Gln Trp Lys Ser
        675                 680                 685

Glu Gly Glu Thr Ser Glu Asp Glu Asp Glu Phe Asp Glu Lys Asn Pro
    690                 695                 700

Ala Ile Val Gln Thr Ala Arg Ser Ser Asp Leu Asn Lys Glu Asn Ser
705                 710                 715                 720

Arg Asn Thr Asn Ile Ser Ser Lys Ile Ala Ser Leu Val Arg Gln Lys
            725                 730                 735

Arg Glu His Glu Lys Lys Glu
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<210> 223
<211> 397
<212> PRT
<213> Saccharomyces sp.

<400> 223
Met Leu His Gln Lys Ile Ala His Lys Val Arg Lys Val Val Pro
 1               5                  10                  15

Gly Ile Ser Leu Leu Ile Phe Phe Gln Gly Cys Leu Ile Leu Leu Phe
                20                  25                  30

Leu Gln Leu Thr Tyr Lys Thr Leu Tyr Cys Arg Asn Asp Ile Arg Lys
        35                  40                  45

Gln Ile Gly Leu Asn Lys Thr Lys Arg Leu Phe Ile Val Leu Val Ser
    50                  55                  60

Ser Ile Leu His Val Val Ala Pro Ser Ala Val Arg Ile Thr Thr Glu
65                  70                  75                  80

Asn Ser Ser Val Pro Lys Gly Thr Phe Phe Leu Asp Leu Lys Lys Lys
                85                  90                  95

Arg Ile Leu Ser His Leu Lys Ser Asn Ser Val Ala Ile Cys Asn His
            100                 105                 110

Gln Ile Tyr Thr Asp Trp Ile Phe Leu Trp Trp Leu Ala Tyr Thr Ser
            115                 120                 125

Asn Leu Gly Ala Asn Val Phe Ile Ile Leu Lys Lys Ser Leu Ala Ser
    130                 135                 140

Ile Pro Ile Leu Gly Phe Gly Met Arg Asn Tyr Asn Phe Ile Phe Met
145                 150                 155                 160

Ser Arg Lys Trp Ala Gln Asp Lys Ile Thr Leu Ser Asn Ser Leu Ala
                165                 170                 175

Gly Leu Asp Ser Asn Ala Arg Gly Ala Gly Ser Leu Ala Gly Lys Ser
            180                 185                 190

Pro Glu Arg Ile Thr Glu Glu Gly Glu Ser Ile Trp Asn Pro Glu Val
        195                 200                 205

Ile Asp Pro Lys Gln Ile His Trp Pro Tyr Asn Leu Ile Leu Phe Pro
    210                 215                 220

Glu Gly Thr Asn Leu Ser Ala Asp Thr Arg Gln Lys Ser Ala Lys Tyr
225                 230                 235                 240

Ala Ala Lys Ile Gly Lys Lys Pro Phe Lys Asn Val Leu Leu Pro His
                245                 250                 255

Ser Thr Gly Leu Arg Tyr Ser Leu Gln Lys Leu Lys Pro Ser Ile Glu
            260                 265                 270

Ser Leu Tyr Asp Ile Thr Ile Gly Tyr Ser Gly Val Lys Gln Glu Glu
            275                 280                 285

Tyr Gly Glu Leu Ile Tyr Gly Leu Lys Ser Ile Phe Leu Glu Gly Lys
    290                 295                 300

Tyr Pro Lys Leu Val Asp Ile His Ile Arg Ala Phe Asp Val Lys Asp
305                 310                 315                 320

Ile Pro Leu Glu Asp Glu Asn Glu Phe Ser Glu Trp Leu Tyr Lys Ile
            325                 330                 335
```

Trp Ser Glu Lys Asp Ala Leu Met Glu Arg Tyr Tyr Ser Thr Gly Ser
            340   345   350

Phe Val Ser Asp Pro Glu Thr Asn His Ser Val Thr Asp Ser Phe Lys
            355   360   365

Ile Asn Arg Ile Glu Leu Thr Glu Val Leu Ile Leu Pro Thr Leu Thr
370   375   380

Ile Ile Trp Leu Val Tyr Lys Leu Tyr Cys Phe Ile Phe
385   390   395

<210> 224
<211> 303
<212> PRT
<213> Saccharomyces sp.

<400> 224
Met Ser Val Ile Gly Arg Phe Leu Tyr Tyr Leu Arg Ser Val Leu Val
  1   5   10   15

Val Leu Ala Leu Ala Gly Cys Gly Phe Tyr Gly Val Ile Ala Ser Ile
            20   25   30

Leu Cys Thr Leu Ile Gly Lys Gln His Leu Ala Gln Trp Ile Thr Ala
            35   40   45

Arg Cys Phe Tyr His Val Met Lys Leu Met Leu Gly Leu Asp Val Lys
     50   55   60

Val Val Gly Glu Glu Asn Leu Ala Lys Lys Pro Tyr Ile Met Ile Ala
 65   70   75   80

Asn His Gln Ser Thr Leu Asp Ile Phe Met Leu Gly Arg Ile Phe Pro
            85   90   95

Pro Gly Cys Thr Val Thr Ala Lys Lys Ser Leu Lys Tyr Val Pro Phe
            100   105   110

Leu Gly Trp Phe Met Ala Leu Ser Gly Thr Tyr Phe Leu Asp Arg Ser
            115   120   125

Lys Arg Gln Glu Ala Ile Asp Thr Leu Asn Lys Gly Leu Glu Asn Val
            130   135   140

Lys Lys Asn Lys Arg Ala Leu Trp Val Phe Pro Glu Gly Thr Arg Ser
145   150   155   160

Tyr Thr Ser Glu Leu Thr Met Leu Pro Phe Lys Lys Gly Ala Phe His
            165   170   175

Leu Ala Gln Gln Gly Lys Ile Pro Ile Val Pro Val Val Val Ser Asn
            180   185   190

Thr Ser Thr Leu Val Ser Pro Lys Tyr Gly Val Phe Asn Arg Gly Cys
            195   200   205

Met Ile Val Arg Ile Leu Lys Pro Ile Ser Thr Glu Asn Leu Thr Lys
            210   215   220

Asp Lys Ile Gly Glu Phe Ala Glu Lys Val Arg Asp Gln Met Val Asp
225   230   235   240

Thr Leu Lys Glu Ile Gly Tyr Ser Pro Ala Ile Asn Asp Thr Thr Leu
            245   250   255

Pro Pro Gln Ala Ile Glu Tyr Ala Ala Leu Gln His Asp Lys Lys Val
            260   265   270

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Asn Lys Lys Ile Lys Asn Glu Pro Val Pro Ser Val Ser Ile Ser Asn
        275                 280                 285
Asp Val Asn Thr His Asn Glu Gly Ser Ser Val Lys Lys Met His
        290                 295                 300
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<210> 225
<211> 1146
<212> DNA
<213> Saccharomyces sp.

<400> 225
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agccccctt ggagatttct ttcatacagt acatcattac tgaccttcgg tgtatcaaaa  120
ctgcttcttt tcacatgcta taatgtcaaa ttgaatggtt ttgaaaaatt agaaactgcc  180
ttggaacgtt ccaaaaggga aaatagaggc cttatgacgg tcatgaacca tatgagtatg  240
gtcgatgatc cgttagtttg ggcaacacta ccatataagt tatttacgtc tttggacaac  300
ataagatggt ctttgggtgc acataatatt tgctttcaaa ataaatttct ggccaacttt  360
ttctcacttg gccaagtcct ttcaacagaa agatttgggg tgggcccatt tcaaggttct  420
atagatgctt caataagatt gttaagccct gacgacactt tagacttgga atggacccct  480
cactctgagg tctcttcttc gctaaaaaaa gcctactccc cgcccataat aaggtcgaag  540
ccatcttggg tccatgttta tccagaagga tttgtactac aattatatcc gccttttgaa  600
aattcgatga ggtatttaa atggggtatt accagaatga tcctagaagc aacaaagccg  660
cccattgtag taccaatatt tgctacaggg tttgaaaaaa tagcatccga agcagtcaca  720
gattcaatgt ttagacaaat tctaccaaga aactttggct ctgaaataaa tgttaccata  780
ggggatcctt taaatgatga tttaatcgac aggtatagaa aagaatggac acatttggtt  840
gaaaaatact atgatcccaa aaatcctaac gacctctctg acgaattgaa atatggtaaa  900
gaggcgcaag atttaagaag cagattagcc gctgaactga gagcccatgt tgctgaaatt  960
agaaatgaag ttcgcaaatt accacgcgaa gaccctaggt tcaaatcccc ctcatggtgg  1020
aagcggttca acaccacgga aggtaaatcg gacccagatg ttaaagtcat tggcgaaaat  1080
tgggcaataa ggaggatgca aaagtttctg cctccagagg gtaaaccaaa gggtaaggat  1140
gattga  1146
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<210> 226
<211> 1191
<212> DNA
<213> Saccharomyces sp.

<400> 226
atgaagcatt cccaaaaata ccgtaggtat ggaatttatg aaaagactgg taatcccttt  60
ataaaagggt tgcaaaggct gcttatcgct tgcttgttca tttcaggctc gctgagtatt  120
gtcgttttc agatctgtct acaggtgctt ctcccttgga gcaagattag atttcaaaat  180
ggtataaatc aaagtaagaa ggctttttatc gttttattat gcatgatctt gaacatggtg  240
gctccctctt ctttgaatgt cacttttgaa acatcgcggc cattgaagaa ctcttctaac  300
gccaagccat gctttagatt taaagacagg gctataataa ttgcaaatca tcaaatgtat  360
gcagactgga tttatctctg gtggctttcc tttgtttcaa atttgggtgg taacgtttat  420
atcatcctga gaaagctct gcagtacata ccattactgg gatttggcat gcgaaatttt  480
aagtttatat ttttaagtag gaactggcaa aaggatgaga aagctttaac aaatagtttg  540
gtttctatgg acttaaacgc gaggtgcaag gggccctta caaattataa gagttgttat  600
tccaagacaa atgaatccat tgccgcttat aatttaatca tgttccctga gggtacaaat  660
ctaagcctca agacaagaga aaaaagcgag gcattctgtc aaagagcaca tttggaccat  720
gtccaattaa gacatttgtt attaccgcac tctaaaggct tgaagtttgc agtagaaaaa  780
ctagctccta gtttagatgc tatctacgat gtcactattg gatattctcc cgccttgaga  840
acggaatacg tcggcaccaa attcaccttg aagaaaatat tcttaatggg tgtctatccg  900
gagaaagtag attttttatat tagggaattt agagttaatg agatcccttt gcaagatgac  960
gaagtttttt tcaattggtt actgggcgtg tggaaagaaa aagatcaact gctagaagac  1020
tactacaaca caggccaatt taaaagtaat gctaaaaatg acaaccaatc catcgttgtt  1080
acgacacaaa cgactggatt tcagcacgaa acattgacac cccgtatcct ttcatattac  1140
gggttcttcg ctttttctat tcttgtattt gtgatgaaaa aaaatcattg a  1191
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<210> 227
<211> 1440
<212> DNA
<213> Saccharomyces sp.

<400> 227
atgggttttg ttgatttctt cgaaacatat atggtcggtt ctagggtcca gttcaaacag  60
ttagatattt ctgattggtt gagtctgacc ccaaggttgc ttattctttt tggctatttt 120
taccttcatt cttttttttac tgcaatcaat caattcctac agttcattaa cacgaattcc 180
ttctgtctta gactgcattt actatatgac agattttggt cgcatgtgcc cataataggt 240
gagtacaaaa ttcggctgct ctcgagggca ctgacatata gtaaactgaa aataatacca 300
actttagaca aggtgctgga ggcgattgaa atttggtttc agctacattt agttgaaatg 360
accttcgaaa aaaaaaaaaa cgtccaaatt ttcataaccg agggaagtga tgacctaaac 420
tttttttaaag atagcaaatt ccaaaccaca ttaatgatat gtaatcatcg atcagtgaat 480
gactacacat tgattaatta ccttttttctc aaaagttgtc ccaccaagtt ttatactaaa 540
tgggaatttc tacaaaagct gaggaagggg gaagatctag ctgaatggcc tcagttaaaa 600
tttcttggtt ggggaaaaat gtttaacttt cctcgattgg atctactaaa gaacatattc 660
ttcaaagatg aaacactcgc actctcatcg aatgagttaa gagatatttt agaaagacaa 720
aacaatcaag ctattactat tttccccgaa gtcaatatca tgagtttgga actatcaatt 780
attcaaagaa aattcacacca agattttccc tttgttataa acttctataa tttattatac 840
ccaagattta aaaactttac cactttgatg gctgctttt catcaattaa aaacatcaaa 900
agaaagaaaa accgtaacaa tataatcaaa gaggcccgat acctgtttca cagagaactt 960
gacaaattag ttcacaagag catgaaaatg gagtcttcca aggtatccga taagacgacg
1020
ccgcccatga tcgtagataa ttcatactta cttacaaaaa aggaagaaat cagcagcggc
1080
aagcccaagg tggtacgaat caatccatac atatatgatg tcaccataat ttattaccga
1140
gtcaaatata ctgatagtgg gcatgatcat accaacggag atttgagact tcataaaggt
1200
tatcaattag agcaaatatc tccgacaatc tttgagatga ttcaaccaga aatggagtct
1260
gaaaacaaca taaaggataa ggaccccatt gttgtgatgg taaatgtaaa aaagcatcaa
1320
attcaaccat tactcgcata caatgatgag agtttagaaa agtggcttga aaataggtgg
1380
atagaaaaag atagattaat cgagtccttg caaaaaaata ttaaaattga gaccaaataa
1440

<210> 228
<211> 903
<212> DNA
<213> Saccharomyces sp.

<400> 228
atggaaaagt acaccaattg gagagacaat ggtacgggaa tagctccatt tctaccaaac  60
acaatcagga aacctagtaa ggtgatgaca gcgtgtttgt tgggtatcct aggggtgaaa 120
accattataa tgctaccatt gattatgctg taccttctaa ctggccagaa caacttactg 180
ggtttgatat tgaagtttac attcagttgg aaagaggaaa ttaccgtgca aggaatcaag 240
aaacgtgacg taaggaaatc caagcattat ccacagaagg gcaagcttta tatttgcaat 300
tgtacctcac cttttagatgc ttttttcagtg gtgttattag ctcaagggcc tgttacgttg 360
ttggtcccat ccaatgacat tgtatacaaa gtttccataa gagaattcat caacttcatc 420
ctcgccggtg ggttagatat aaaactctat ggccacgagg tagcagagct atctcaattg 480
ggcaataccg tgaattttat gtttgctgag ggtacctcat gtaatggtaa aagcgtctta 540
ccgtttagta taaccgggaa aaaacttaaa gaattcatag acccttcaat aaccacaatg 600
aacccccgcaa tggccaaaac taaaaaattt gaattgcaga ccatccaaat caaaactaat 660
aaaactgcca tcaccacatt gcccatctcc aatatggagt atttatctag atttctgaac 720
aagggcatta atgttaaatg caagatcaac gagccacaag tactctcgga taatttagag 780
gaattacgcg ttgcattaaa cggtggcgac aaatataaac tagtctcacg gaagttagat 840
gttgaatcta agaggaattt tgtgaaggaa tatatcagcg atcaacgtaa aaagaggaag 900
tag                                                                903

<210> 229
<211> 2280
<212> DNA
<213> Saccharomyces sp.

<400> 229
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aattacagtt ccatcgaggc caaaagcgtc aagacgtcgg ctgatcaggc atacatctac 120
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caagagccta gcgctaccaa gaagatactt tactccatcg ccacatggct gttgtacaac 180
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ggaccggtga tctttgttgc ggctccgcat gctaaccagt tcgtcgaccc tgtaatcctt 300
atgggcgagg tgaagaaatc tgtcaacaga cgtgtgtcct tcttgattgc ggagagctca 360
ttaaagcaac cccccatagg gttttttggct agtttcttca tggccatagg cgtggtaagg 420
ccgcaggata atttgaaacc ggcagaaggt actatccgcg tagatccaac agactacaag 480
agagttatcg gccacgacac gcatttcttg actgattgta tgccaaaggg tctcatcggg 540
ttacccaaat caatgggatt tggagaaatc cagtccatag aaagtgacac gagtttgacc 600
ctaagaaaag agttcaaaat ggccaaacca gagattaaaa ctgctttact caccggcact 660
acttataaat atgccgctaa agtcgaccaa tcttgcgttt accatagagt ttttgagcat 720
ttggcccata acaactgcat tgggatcttt cctgaaggtg ggtcccacga cagaacaaac 780
ttgttgcccc tgaaagcagg tgtgccgatt atggctcttg gttgcatgga taagcatcct 840
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taccacaacc cggaaacgaa cagagatgca gtgaaagaat tattagatac catatcgaag
1020
ggtttacaat ccgttaccgt tacatgttct gattatgaaa ctttgatggt ggttcaaacg
1080
ataagaagac tatatatgac acaatttagc accaagttac cgttgccctt gattgtggaa
1140
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1200
ttgaccaaag atataatggc atataatgcc gccttgagac actataatct tcctgatcac
1260
cttgtggagg aggcaaaggt aaatttcgca aaaaacctcg gacttgtttt ttttagatcc
1320
atcgggctct gcatcctctt ttcgttagcc atgccaggta tcattatgtt ctcacctgtc
1380
ttcatattag ccaagagaat ttctcaagaa aaggcccgta ccgctttgtc caagtctaca
1440
gttaaaataa aggctaacga tgtcattgcc acgtggaaaa tcttgattgg gatgggattt
1500
gcgcccttgc tttacatctt ttggtccgtt ttaatcactt attacctcag acataaacca
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1680
tctcttacat ctccaaaggg cttgcaaaag ctacaaaagg atcgtagaaa tctggcagaa
1740
agaataatcg aagttgtaaa taactttgga agcgaattat tccccgattt cgatagtgcc
1800
gccctacgtg aagaattcga cgtcatcgat gaagaggaag aagatcgaaa aacctcagaa
1860
ttgaatcgca ggaaaatgct aagaaaacag aaaataaaaa gacaagaaaa agattcgtca
1920
tcacctatca tcagccaacg tgacaaccac gatgcctatg aacaccataa ccaagattcc
1980
gatggcgtct cattggtcaa tagtgacaat tccctctcta acattccatt attctcttct
2040
acttttcatc gtaagtcaga gtcttcctta gcttcgacat ccgttgcacc ttcttcttcc
2100
tccgaatttg aggtagaaaa cgaaatcttg gaggaaaaaa atggattagc aagtaaaatc
2160
gcacaggccg tcttaaacaa gagaattggt gaaaatactg ccagggaaga ggaagaggaa
2220
gaagaagagg aagaagaaga agaggaagaa gaagaagaag ggaaagaagg agatgcgtag
2280
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<210> 230
<211> 2232
<212> DNA
<213> Saccharomyces sp.

<400> 230
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tcccgacggt acaaaaattc atacaatgga ttcgtataca atatacatac atggctgtat 120
gatgtgtctg tatttctgtt taatattttg ttcactattt tcttcagaga aattaaggta 180
cgtggtgcat ataacgttcc cgaagttggg gtgccaacca tccttgtgtg tgcccctcat 240
gcaaatcagt tcatcgaccc ggctttggta atgtcgcaaa cccgtttgct gaagacatca 300
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gcgggaaagt cccgatccag aatgccttgt tttgttactg ctgagtcgag ttttaagaaa 360
agatttatct ctttctttgg tcacgcaatg ggcggtattc ccgtgcctag aattcaggac 420
aacttgaagc cagtggatga gaatcttgag atttacgctc cggacttgaa gaaccacccg 480
gaaatcatca agggccgctc caagaaccca cagactacac cagtgaactt tacgaaaagg 540
ttttctgcca agtccttgct tggattgccc gactacttaa gtaatgctca aatcaaggaa 600
atcccggatg atgaaacgat aatcttgtcc tctccattca gaacatcgaa atcaaaagtg 660
gtggagctct tgactaatgg tactaatttt aaatatgcag agaaaatcga caatacggaa 720
actttccaga gtgttttttga tcacttgcat acgaagggct gtgtaggtat tttccccgag 780
ggtggttctc atgaccgtcc ttcgttacta cccatcaagg caggtgttgc cattatggct 840
ctgggcgcag tagccgctga tcctaccatg aaagttgctg ttgtacccctg tggtttgcat 900
tatttccaca gaaataaatt cagatctaga gctgtttttag aatacggcga acctatagtg 960
gtggatggga aatatggcga aatgtataag gactccccac gtgagaccgt ttccaaacta
1020
ctaaaaaaga tcaccaattc tttgtttttct gttaccgaaa atgctccaga ttacgatact
1080
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1140
cctgccattg tagaaatcaa cagaaggtta cttttcggtt attccaagtt taaagatgat
1200
ccaagaatta ttcacttaaa aaaactggta tatgactaca acaggaaatt agattcagtg
1260
ggtttaaaag accatcaggt gatgcaatta aaaactacca aattagaagc attgaggtgc
1320
tttgtaactt tgatcgttcg attgattaaa ttttctgtct ttgctatact atcgttaccg
1380
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1440
aaagagggtt aaagaaatc attggttaaa attaagggta ccgatttgtt ggccacatgg
1500
aaacttatcg tggcgttaat attggcacca atttttatacg ttacttactc gatcttgttg
1560
attattttgg caagaaaaca acactattgt cgcatctggg ttccttccaa taacgcattc
1620
atacaatttg tctattttta tgcgttattg gttttcacca cgtattcctc tttaaagacc
1680
ggtgaaatcg gtgttgacct tttcaaatct ttaagaccac tttttgtttc tattgtttac
1740
cccggtaaga agatcgaaga aatccaaaca acaagaaaga atttaagtct agagttgact
1800
gctgtttgta cgatttagg acctttggtt ttccctgatt acgataaatt agcgactgag
1860
atattctcta agagagacgg ttatgatgtc tcttctgatg cagagtcttc tataagtcgt
1920
atgagtgtac aatctagaag ccgctcttct tctatacatt ctattggctc gctagcttct
1980
aacgccctat caagagtgaa ttcaagaggc tcgttgaccg atattccaat tttttctgat
2040
gcaaagcaag gtcaatggaa aagtgaaggt gaaactagtg aggatgagga tgaatttgat
2100
gagaaaaatc ctgccatagt acaaaccgca cgaagttctg atctaaataa ggaaaacagt
2160
cgcaacacaa atatatcttc gaagattgct tcgctggtaa gacagaaaag agaacacgaa
2220
aagaaagaat ga
2232
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<210> 231
<211> 1194
<212> DNA
<213> Saccharomyces sp.

<400> 231
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tactgtagaa atgatataag gaaacaaatt ggtctcaata aaaccaaaag attatttatt 180
gtcttggtat catccatttt gcatgttgtc gcaccatctg cagtgagaat taccactgaa 240
aattccagtg ttcctaaagg tactttttttt ttagacttga agaagaaaag gattctttct 300
catctaaagt ccaattcggt ggccatttgc aatcaccaaa tatacacgga ttggatattt 360
ttatggtggt tggcttacac atcgaactta ggggctaatg tcttcattat tttaaaaaaa 420
tcgttggctt ccattcctat cctcggtttc ggtatgagaa actataattt cattttttatg 480
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agtagaaagt gggcacaaga caaaataacc ctaagcaaca gccttgctgg ccttgattcg 540
aatgcaaggg gcgccggctc acttgctgga aagtcacctg agcgcataac tgaggaagga 600
gagagcatat ggaatccgga ggttattgat ccaaaacaaa tccattggcc atacaatctt 660
atcctattcc ctgaaggtac aaatctcagt gctgatacta ggcaaaaaag tgctaaatat 720
gctgccaaaa taggcaaaaa gccattcaag aatgtgctac tgcctcattc tacaggccta 780
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tactccggtg taaaacagga ggaatatggt gagcttatat atgggctgaa gagcatattt 900
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1080
cattcagtta ccgatagttt caagatcaat cgtattgagt taactgaagt gctaatatta
1140
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1194
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<210>  232
<211>  912
<212>  DNA
<213>  Saccharomyces sp.

<400>  232
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catttggctc agtggattac tgcgcgttgt ttttaccatg tcatgaaatt gatgcttggc 180
cttgacgtca aggtcgttgg cgaggagaat ttggccaaga agccatatat tatgattgcc 240
aatcaccaat ccaccttgga tatcttcatg ttaggtagga tttttccccc tggttgcaca 300
gttactgcca agaagtcttt gaaatacgtc ccctttctgg gttggttcat ggctttgagt 360
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ttagaaaatg ttaagaaaaa caagcgtgct ctatgggttt ttcctgaggg taccaggtct 480
tacacgagtg agctgacaat gttgcctttc aagaagggtg ctttccattt ggcacaacag 540
ggtaagatcc ccattgttcc agtggttgtt ccaatacca gtactttagt aagtcctaaa 600
tatggggtct tcaacagagg ctgtatgatt gttagaattt aaaacctat ttcaaccgag 660
aacttaacaa aggacaaaat tggtgaattt gctgaaaaag ttagagatca aatggttgac 720
actttgaagg agattggcta ctctcccgcc atcaacgata caaccctccc accacaagct 780
attgagtatg ccgctcttca acatgacaag aaagtgaaca agaaaatcaa gaatgagcct 840
gtgccttctg tcagcattag caacgatgtc aatacccata acgaaggttc atctgtaaaa 900
aagatgcatt aa 912
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<210>  233
<211>  54
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:Synthetic
       Oligonucleotide

<400>  233
cgcgatttaa atggcgcgcc ctgcaggcgg ccgcctgcag ggcgcgccat ttaa         54
```

```
<210>  234
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:Synthetic
       Oligonucleotide

<400>  234
tcgaggatcc gcggccgcaa gcttcctgca gg                                 32
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<210>  235
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
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<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

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<210> 236
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 236
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<210> 237
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 238
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
     Oligonucleotide

<400> 238
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<210> 239
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
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<210> 240
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
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<210> 241
<211> 28
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 241
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